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|------|----------------------------|---|--|--------------|--|
| 2858 | 80049806 (11691, 11692) | Novel Protein sim. GBank gi 3122879 sp O07438 SYA_MYCTU - ALANYL- tRNA SYNTHETASE (ALANINE--tRNA LIGASE) (ALARS) | Contains protein domain (PF01411) - tRNA synthetases class II (A) | UNCLASSIFIED | 1004, 1010, 1012, 1016, 1034, 1039, 1044 |
| 2859 | 80022287 (16637, 16638) | Novel Protein sim. GBank gi 3122886 sp O34526 SYA_BACSU - ALANYL- tRNA SYNTHETASE (ALANINE--tRNA LIGASE) (ALARS) | Contains protein domain (PF01411) - tRNA synthetases class II (A) | UNCLASSIFIED | 1004 |
| 2860 | 86473928 (11009, 11010) | Novel Protein sim. GBank gi 419757 pir S30145 - ketol-acid reductoisomerase (EC 1.1.1.86) precursor - Arabidopsis thaliana | Contains protein domain (PF01450) - Acetylhydroxy acid isomerase/reductase | UNCLASSIFIED | 1003, 1008, 1053, 1054 |
| 2861 | 79835057 (12141, 12142) | Novel Protein sim. GBank gi 4204413 (AF047001) - Lys44 [Oenococcus oeni temperate bacteriophage fOg44] | Contains protein domain (PF01476) - Putative peptidoglycan binding domain | UNCLASSIFIED | 1039 |
| 2862 | 20438269 (11797, 11798) | Novel Protein sim. GBank gi 728840 sp P39046 ALYS_ENTHR - AUTOLYSIN PRECURSOR (N- ACETYL MURAMOYL-L-ALANINE AMIDASE) (MURAMIDASE-2) | Contains protein domain (PF01476) - Putative peptidoglycan binding domain | UNCLASSIFIED | 1010 |
| 2863 | 86684852 (11347, 11348) | Novel Protein sim. GBank gi 2326738 emb CAB10952 - (Z98268) hypothetical protein Rv1695 [Mycobacterium tuberculosis] | Contains protein domain (PF01513) - Domain of unknown function | UNCLASSIFIED | 1001, 1004, 1006, 1008, 1010, 1012, 1018, 1019, 1022, 1024, 1025, 1026, 1027, 1029, 1030, 1031, 1034, 1038, 1039, 1053, 1054 |
| 2864 | 17938848 (11943, 11944) | Novel Protein sim. GBank gi 154916 (M95402) - transposase [Transposon Tn5393] | Contains protein domain (PF01526) - Transposase | UNCLASSIFIED | 1039 |
| 2865 | 57292642 (11273, 11274) | Novel Protein sim. GBank gi 1176580 sp P42836 YN66_YEAST - HYPOTHETICAL 39.2 KD PROTEIN IN EG12- KRE1 INTERGENIC REGION | Contains protein domain (PF01529) - DHHC zinc finger domain | UNCLASSIFIED | 1004, 1006, 1017, 1022, 1024, 1034 |

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| 2866 | 80430268 (5135, 5136) | Novel Protein sim. GBank g 1666161 emb CAB03772] - (281451) hypothetical protein Rv242c [Mycobacterium tuberculosis] | Contains protein domain (PF01548) - Transposase | UNCLASSIFIED | 1026, 1038, 1044 |
| 2867 | 78673180 (9287, 9288) | Novel Protein sim. GBank g 4980710 gb AAD35304.1 AE00170 - (AE001706) glycine cleavage system H protein [Thermotoga maritima] | Contains protein domain (PF01597) - Glycine cleavage H-protein | UNCLASSIFIED | 1026, 1039 |
| 2868 | 87139316 (977, 978) | Novel Protein sim. GBank g 3452358 (AF075724) - legiolysin [Legionella pneumophila] | Contains protein domain (PF01626) - 4-hydroxyphenylpyruvate dioxygenase C terminal domain | UNCLASSIFIED | 1010 |
| 2869 | 85801185 (17125, 17126) | Novel Protein sim. GBank g 3452358 (AF075724) - legiolysin [Legionella pneumophila] | Contains protein domain (PF01626) - 4-hydroxyphenylpyruvate dioxygenase C terminal domain | UNCLASSIFIED | 1025 |
| 2870 | 20726398 (7365, 7366) | Novel Protein sim. GBank g 729312 sp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRBOMUTASE) | Contains protein domain (PF01676) - Metalloenzyme superfamily | UNCLASSIFIED | 1006 |
| 2871 | 82060992 (10487, 10488) | Novel Protein sim. GBank g 249878 sp Q03674 PLB2_YEAST - PUTATIVE LYSOPHOSPHOLIPASE PRECURSOR (PHOSPHOLIPASE B) | Contains protein domain (PF01735) - Lysophospholipase catalytic domain | UNCLASSIFIED | 1000, 1001, 1003, 1004, 1006, 1008, 1009, 1012, 1016, 1022, 1023, 1024, 1025, 1026, 1034, 1039, 1044 |
| 2872 | 78041806 (11655, 11656) | Novel Protein sim. GBank g 2293162 (AF008220) - putative peptidase [Bacillus subtilis] | Contains protein domain (PF01738) - Diene lactone hydrolase family | UNCLASSIFIED | 1044 |
| 2873 | 78484530 (2565, 2566) | Novel Protein sim. GBank g 2833223 sp Q12460 SIK1_YEAST - SIK1 PROTEIN | Contains protein domain (PF01798) - Putative snoRNA binding domain | UNCLASSIFIED | 1009 |

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| 2874 | 81590727 (20343) 20344) | Novel Protein sim. GBank gil2739100 (AF027507) - primase [Mycobacterium smegmatis] | Contains protein domain (PF01807) - CHC2 zinc finger | UNCLASSIFIED | 1054 |
| 2875 | 65452252 (5305, 5306) | Novel Protein sim. GBank gil202857 (M77183) - alpha-1-macroglobulin [Rattus norvegicus] | Contains protein domain (PF01835) - Alpha-2-macroglobulin family N-terminal region | UNCLASSIFIED | 1016, 1044 |
| 2876 | 11767889 (10623, 10624) | Novel Protein sim. GBank gil1731343[sp Q10694 YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY49.25] | Contains protein domain (PF01836) - Transposase | UNCLASSIFIED | 1022 |
| 2877 | 86685844 (18489, 18490) | Novel Protein sim. GBank gil95567[pir S2 562 - hypothetical protein B - Erwinia amylovora | Contains protein domain (PF01836) - Transposase | UNCLASSIFIED | 1029 |
| 2878 | 17960637 (21695, 21696) | Novel Protein sim. GBank gil1460074[emb CAB01049] - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis] | Contains protein domain (PF01841) - Transglutaminase-like superfamily | UNCLASSIFIED | 1016 |
| 2879 | 80258861 (18249, 18250) | Novel Protein sim. GBank gil1518779 (J62581) - phenylalanine hydroxylase gene cluster transcription activator PhhR [Pseudomonas aeruginosa] | Contains protein domain (PF01842) - ACT domain | UNCLASSIFIED | 1034 |
| 2880 | 78465452 (11555, 11556) | Novel Protein sim. GBank gil188864 (M74027) - mucin [Homo sapiens] | Contains protein domain (PF01844) - HNH endonuclease | UNCLASSIFIED | 1003 |
| 2881 | 13883332 (15093, 15094) | Novel Protein sim. GBank gil2314032[gb AAD07943.1 - (AE0000599) outer membrane protein (omp19) [Helicobacter pylori 26695] | Contains protein domain (PF01856) - Outer membrane protein | UNCLASSIFIED | 1053 |
| 2882 | 79827273 (21911, 21912) | Novel Protein sim. GBank gil3261828[emb CAB10925 - (Z98260) mfp [Mycobacterium tuberculosis] | Contains protein domain (PF01883) - Domain of unknown function | UNCLASSIFIED | 1004, 1017, 1031, 1044, 1049 |

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| 2883 | 80431264 (20381, 20382) | Novel Protein sim. GBank gi 7314361 sp P40010 YEJ6_YEAST - HYPOTHETICAL GTP-BINDING PROTEIN IN PM140-PAC2 INTERGENIC REGION | Contains protein domain (PF01926) - GTPase of unknown function | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1010, 1012, 1017, 1022, 1023, 1024, 1026, 1034, 1036, 1038, 1044, 1054 |
| 2884 | 78052499 (2561, 2562) | Novel Protein sim. GBank gi 1722971 sp Q10634 Y036_MYCTU - HYPOTHETICAL 25.1 KD PROTEIN CY130.06 | Contains protein domain (PF01939) - Protein of unknown function | UNCLASSIFIED | 1026 |
| 2885 | 19882099 (14089, 14090) | Novel Protein sim. GBank gi 3250916 embj CAA07434 - (AJ007291) CAP1 [Rattus norvegicus] | Contains protein domain (PF01965) - Thio/Pip family | UNCLASSIFIED | 1022 |
| 2886 | 81183403 (21255, 21256) | Novel Protein sim. GBank gi 2634068 emb CAB13569 - (Z99112) similar to hypothetical proteins [Bacillus subtilis] | Contains protein domain (PF01966) - HD domain | UNCLASSIFIED | 1004, 1022, 1054 |
| 2887 | 80230242 (19107, 19108) | Novel Protein sim. GBank gi 1001236 dbj BAA10477 - (D64003) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1031 |
| 2888 | 20465177 (1757, 1758) | Novel Protein sim. GBank gi 1001423 dbj BAA10046 - (D63999) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1010 |
| 2889 | 10880972 (12769, 12770) | Novel Protein sim. GBank gi 1001642 dbj BAA10373 - (D64002) dGTP triphosphohydrolase [Synechocystis sp.] | | UNCLASSIFIED | 1038 |
| 2890 | 94684783 (1905, 1906) | Novel Protein sim. GBank gi 1001663 dbj BAA10397 - (D64002) rare lipoprotein A [Synechocystis sp.] | | UNCLASSIFIED | 1010, 1022 |
| 2891 | 52561021 (83, 84) | Novel Protein sim. GBank gi 1001693 dbj BAA10430 - (D64002) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1017 |
| 2892 | 79427000 (16341, 16342) | Novel Protein sim. GBank gi 1001693 dbj BAA10430 - (D64002) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1017 |

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| 2893 | 65981968 (7597, 7598) | Novel Protein sim. GBank gil 10086608[dbj]BAA10762] - (D64005) pyridoxal phosphate biosynthetic protein FdxA [Synechocystis sp.] | | UNCLASSIFIED | 1024 |
| 2894 | 10371303 (18035, 18036) | Novel Protein sim. GBank gil 102424 pir A41132 - collagen-related protein 1 precursor - Hydra magnipapillata | | UNCLASSIFIED | 1017 |
| 2895 | 27837744 (9015, 9016) | Novel Protein sim. GBank gil 102425 pir B41132 - collagen-related protein 2 - Hydra magnipapillata (fragment) | | UNCLASSIFIED | 1053 |
| 2896 | 78965883 (4683, 4684) | Novel Protein sim. GBank gil 102426 pir C41132 - collagen-related protein 3 precursor - Hydra magnipapillata | | UNCLASSIFIED | 1030, 1054 |
| 2897 | 80078979 (4711, 4712) | Novel Protein sim. GBank gil 104266 pir B38274 - Y-box protein 2 - African clawed frog | | UNCLASSIFIED | 1034 |
| 2898 | 20294734 (4227, 4228) | Novel Protein sim. GBank gil 1044963 bbs 169846 - protamine [Monodonta turbinata, gonads, Peptide, 106 aa] | | UNCLASSIFIED | 1034 |
| 2899 | 27843855 (11649, 11650) | Novel Protein sim. GBank gil 1044963 bbs 169846 - protamine [Monodonta turbinata, gonads, Peptide, 106 aa] | | UNCLASSIFIED | 1022 |
| 2900 | 80077428 (21831, 21832) | Novel Protein sim. GBank gil 1044963 bbs 169846 - protamine [Monodonta turbinata, gonads, Peptide, 106 aa] | | UNCLASSIFIED | 1034 |
| 2901 | 78732189 (8961, 8962) | Novel Protein sim. GBank gil 1050466 emb CAA62931 - (X91821) dsdC [Escherichia coli] | | UNCLASSIFIED | 1008 |
| 2902 | 21433573 (16759, 16760) | Novel Protein sim. GBank gil 1055163 gb AAA81132.1 - (U40029) Contains similarity to Pfam domain: PF01060 (Worm_family_2), Score=203.8, E-value=8.6e-58, N=1 [Caenorhabditis elegans] | | UNCLASSIFIED | 1024 |
| 2903 | 20728042 (5113, 5114) | Novel Protein sim. GBank gil 1060876 dbj BAA11236 - (D78168) EmrK [Escherichia coli] | | UNCLASSIFIED | 1006 |

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| 2904 | 49613196 (8343, 8344) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1036 |
| 2905 | 65706415 (12013, 12014) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1038 |
| 2906 | 78373241 (19887, 19888) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1009 |
| 2907 | 27348989 (20517, 20518) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1026 |
| 2908 | 19484846 (21275, 21276) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1016 |
| 2909 | 20286419 (11423, 11424) | Novel Protein sim. GBank gil106323 pir A34087 - hypothetical protein (L1H 5' region) - human | | UNCLASSIFIED | 1022 |
| 2910 | 79632735 (8897, 8898) | Novel Protein sim. GBank gil1064791 dbj BAA11277 - (D78193) yydE [Bacillus subtilis] | | UNCLASSIFIED | 1023 |
| 2911 | 39518435 (7585, 7586) | Novel Protein sim. GBank gil1065941 (U40799) - F42C5.7 gene product [Caenorhabditis elegans] | | UNCLASSIFIED | 1024 |
| 2912 | 79179027 (13467, 13468) | Novel Protein sim. GBank gil107284 pir S52856 - AraC-like protein - Azorhizobium caulinodans | | UNCLASSIFIED | 1027 |
| 2913 | 79761936 (2065, 2066) | Novel Protein sim. GBank gil1073072 pir C55543 - cmal protein - Pseudomonas syringae pv. syringae | | UNCLASSIFIED | 1023 |
| 2914 | 13517991 (16239, 16240) | Novel Protein sim. GBank gil1073504 pir S47741 - hypothetical protein o323 - Escherichia coli | | UNCLASSIFIED | 1024 |
| 2915 | 10237747 (19955, 19956) | Novel Protein sim. GBank gil107422 pir B36298 - proline-rich protein PRB3S (cys) - human (fragment) | | UNCLASSIFIED | 1025 |

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| 2916 | 80238540 (6547, 6548) | Novel Protein sim. GBank g 1076211 pir S50755 - deoxyribose-phosphate aldolase (EC 4.1.2.4) - <i>Bacillus subtilis</i> | UNCLASSIFIED | 1004, 1031, 1040 |
| 2917 | 35019572 (983, 984) | Novel Protein sim. GBank g 1076205 pir S50754 - hypothetical protein WP6 - <i>Chlamydomonas eugametos</i> | UNCLASSIFIED | 1016 |
| 2918 | 80046339 (1109, 1110) | Novel Protein sim. GBank g 1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i> | UNCLASSIFIED | 1023, 1024 |
| 2919 | 94139904 (3523, 3524) | Novel Protein sim. GBank g 1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i> | UNCLASSIFIED | 1001, 1003, 1004, 1010, 1022, 1023, 1024, 1034 |
| 2920 | 47654638 (14149, 14150) | Novel Protein sim. GBank g 1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i> | UNCLASSIFIED | 1029 |
| 2921 | 80497394 (18175, 18176) | Novel Protein sim. GBank g 1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i> | UNCLASSIFIED | 1012 |
| 2922 | 23291231 (22479, 22480) | Novel Protein sim. GBank g 1076211 pir S50755 - hypothetical protein VSP-3 - <i>Chlamydomonas reinhardtii</i> | UNCLASSIFIED | 1003 |
| 2923 | 82384772 (1849, 1850) | Novel Protein sim. GBank g 1077044 pir S53485 - carnitine O-acetyltransferase (EC 2.3.1.7), mitochondrial - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1026, 1027, 1031, 1034, 1038, 1039, 1044, 1054 |

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| 2924 | 88094563 (3765, 3766) | Novel Protein sim. GBank gil1077044 pir S532485 - carnitine O-acetyltransferase (EC 2.3.1.7), mitochondrial - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1004, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1025, 1026, 1027, 1029, 1031, 1034, 1039, 1044, 1054 |
| 2925 | 28996027 (3373, 3374) | Novel Protein sim. GBank gil1077164 pir S52500 - SWH1 protein homolog YDL019c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1044 |
| 2926 | 78673811 (1701, 1702) | Novel Protein sim. GBank gil1077187 pir S49777 - probable membrane protein YDR180w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1026 |
| 2927 | 30672500 (871, 872) | Novel Protein sim. GBank gil1077350 pir S50381 - probable membrane protein YLR297w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1008 |
| 2928 | 79842541 (4119, 4120) | Novel Protein sim. GBank gil1077351 pir S50380 - probable membrane protein YLR296w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1008, 1022, 1024 |
| 2929 | 296684825 (1861, 1862) | Novel Protein sim. GBank gil1077356 pir S51378 - probable membrane protein YLR360w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1009 |
| 2930 | 80236763 (6389, 6390) | Novel Protein sim. GBank gil1077393 pir S51403 - probable membrane protein YLR266c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1009, 1010, 1017, 1024, 1025, 1044 |

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| 2931 | 79763658 (5905, 5906) | Novel Protein sim. GBank gil1077404 pir S51422 - probable membrane protein YLR177w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1006, 1008, 1010, 1012, 1022, 1024, 1029, 1034, 1038, 1049 |
| 2932 | 84453120 (4749, 4750) | Novel Protein sim. GBank gil1077407 pir S51435 - hypothetical protein YLR190w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1006, 1044 |
| 2933 | 80245522 (16821, 16822) | Novel Protein sim. GBank gil1077408 pir S51424 - hypothetical protein YLR179c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1017, 1044 |
| 2934 | 27365573 (2485, 2486) | Novel Protein sim. GBank gil1077412 pir S51432 - hypothetical protein YLR187w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1006, 1044 |
| 2935 | 29360701 (8009, 8010) | Novel Protein sim. GBank gil1077523 pir S51252 - probable membrane protein YDR101c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1009 |
| 2936 | 79242196 (15781, 15782) | Novel Protein sim. GBank gil1077539 pir S52698 - hypothetical protein YDR190c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1017, 1044 |
| 2937 | 80222249 (22589, 22590) | Novel Protein sim. GBank gil1077575 pir S52682 - hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1004, 1010, 1024, 1044 |
| 2938 | 17395052 (7195, 7196) | Novel Protein sim. GBank gil1078074 pir S53405 - probable membrane protein YLR328w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1039 |
| 2939 | 79111065 (267, 268) | Novel Protein sim. GBank gil1078086 pir S53412 - probable membrane protein YLR425w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1017 |
| 2940 | 21147788 (11029, 11030) | Novel Protein sim. GBank gil1082211 pir A55575 - ankyrin 3, long form - human | | UNCLASSIFIED | 1058 |

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| 2941 | 19533783 (20697, 20698) | Novel Protein sim. GBank g 1082604 pir S53363 - mucin 5AC (clone JER58) - human (fragment) | | UNCLASSIFIED | 1025 |
| 2942 | 36998752 (19063, 19064) | Novel Protein sim. GBank g 1083739 pir A55163 - nucleolar protein Nopp140, hepatic - rat | | UNCLASSIFIED | 1001 |
| 2943 | 28393356 (21781, 21782) | Novel Protein sim. GBank g 1083764 pir B48013 - proline-rich proteoglycan 2 precursor, parotid - rat | | UNCLASSIFIED | 1017 |
| 2944 | 87113994 (5821, 5822) | Novel Protein sim. GBank g 1084141 pir JX0360 - Na+/H+ antiporter NhaA - Vibrio parahaemolyticus | | UNCLASSIFIED | 1048 |
| 2945 | 79573623 (11197, 11198) | Novel Protein sim. GBank g 1084141 pir JX0360 - Na+/H+ antiporter NhaA - Vibrio parahaemolyticus | | UNCLASSIFIED | 1001 |
| 2946 | 20715380 (1303, 1304) | Novel Protein sim. GBank g 1084649 pir S555965 - probable membrane protein YLR409c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 2947 | 80234823 (13763, 13764) | Novel Protein sim. GBank g 1084649 pir S555965 - probable membrane protein YLR409c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1008, 1038 |
| 2948 | 80230802 (9219, 9220) | Novel Protein sim. GBank g 1084783 pir S54079 - BRR1 protein - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1001, 1009, 1024, 1039 |
| 2949 | 79876174 (12467, 12468) | Novel Protein sim. GBank g 109750 emb CAA90900 - (Z54195) TieB protein [Escherichia coli] | | UNCLASSIFIED | 1017 |
| 2950 | 79623784 (15229, 15230) | Novel Protein sim. GBank g 110587 bbs 170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.] | | UNCLASSIFIED | 1022, 1023 |
| 2951 | 65882631 (3067, 3068) | Novel Protein sim. GBank g 111816 pir S21348 - probable polyprotein-related protein 4 - rat | | UNCLASSIFIED | 1054 |

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| 2952 | 29905721 (14623, 14624) | Novel Protein sim. GBank gil111816 sp P21348 - probable polyprotein-related protein 4 - rat | | UNCLASSIFIED | 1030 |
| 2953 | 90995101 (6373, 6374) | Novel Protein sim. GBank gil1123052 (U41994) - similar to glycoproteins [Caenorhabditis elegans] | | UNCLASSIFIED | 1009, 1010, 1020, 1026, 1034, 1038, 1039 |
| 2954 | 12694385 (5565, 5566) | Novel Protein sim. GBank gil112785 sp P051003MG1_ECOLI - DNA-3- METHYLADENINE GLYCOSIDASE I (3- METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG.) | | UNCLASSIFIED | 1031 |
| 2955 | 79245890 (22769, 22770) | Novel Protein sim. GBank gil113158 sp P25516 ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO- LYASE 1) (ACONITASE 1) | | UNCLASSIFIED | 1039 |
| 2956 | 21433552 (12805, 12806) | Novel Protein sim. GBank gil113632 dbj BA11482 - (D79987) similar to Schizosaccharomyces pombe cut1+ protein which regulates spindle pole body duplication. [Homo sapiens] | | UNCLASSIFIED | 1022 |
| 2957 | 14973768 (10539, 10540) | Novel Protein sim. GBank gil113641 sp P10177 ALKH_ECOLI - 4-HYDROXY 2-OXOGLUTARATE ALDOLASE (2-KETO-4- HYDROXYGLUTARATE ALDOLASE) (KHG- ALDOLASE) / 2-DEHYDRO-3- DEOXYPHOSPHOGLUCONATE ALDOLASE (PHOSPHO-2-DEHYDRO-3- DEOXYGLUCONATE ALDOLASE) (PHOSPHO-2- KETO-3-DEOXYGLUCONATE ALDOLASE) (...) | | UNCLASSIFIED | 1024 |
| 2958 | 78439509 (11151, 11152) | Novel Protein sim. GBank gil113666 sp P23959 ALUA_HUMAN - !!! ALU CLASS A WARNING ENTRY !!! | | UNCLASSIFIED | 1008 |
| 2959 | 27367421 (16137, 16138) | Novel Protein sim. GBank gil113666 sp P23959 ALUA_HUMAN - !!! ALU CLASS A WARNING ENTRY !!! | | UNCLASSIFIED | 1026 |

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| 2960 | 27980277 (21435, 21436) | Novel Protein sim. GBank g 113666 sp P23959 ALUA_HUMAN - !!! ALU CLASS A WARNING ENTRY !!!! | | UNCLASSIFIED | 1022 |
| 2961 | 55174715 (22017, 22018) | Novel Protein sim. GBank g 113666 sp P23959 ALUA_HUMAN - !!! ALU CLASS A WARNING ENTRY !!!! | | UNCLASSIFIED | 1026 |
| 2962 | 90933051 (12747, 12748) | Novel Protein sim. GBank g 113667 sp P23960 ALUB_HUMAN - !!! ALU CLASS B WARNING ENTRY !!!! | | UNCLASSIFIED | 1049 |
| 2963 | 49604227 (2589, 2590) | Novel Protein sim. GBank g 113668 sp P23961 ALUC_HUMAN - !!! ALU CLASS C WARNING ENTRY !!!! | | UNCLASSIFIED | 1036 |
| 2964 | 78792083 (9973, 9974) | Novel Protein sim. GBank g 113668 sp P23961 ALUC_HUMAN - !!! ALU CLASS C WARNING ENTRY !!!! | | UNCLASSIFIED | 1017 |
| 2965 | 91236588 (11641, 11642) | Novel Protein sim. GBank g 113668 sp P23961 ALUC_HUMAN - !!! ALU CLASS C WARNING ENTRY !!!! | | UNCLASSIFIED | 1045 |
| 2966 | 324440873 (11811, 11812) | Novel Protein sim. GBank g 113668 sp P23961 ALUC_HUMAN - !!! ALU CLASS C WARNING ENTRY !!!! | | UNCLASSIFIED | 1000 |
| 2967 | 78377465 (12265, 12266) | Novel Protein sim. GBank g 113668 sp P23961 ALUC_HUMAN - !!! ALU CLASS C WARNING ENTRY !!!! | | UNCLASSIFIED | 1016, 1044 |
| 2968 | 65471910 (18537, 18538) | Novel Protein sim. GBank g 113668 sp P23961 ALUC_HUMAN - !!! ALU CLASS C WARNING ENTRY !!!! | | UNCLASSIFIED | 1054 |
| 2969 | 79257936 (22457, 22458) | Novel Protein sim. GBank g 113668 sp P23961 ALUC_HUMAN - !!! ALU CLASS C WARNING ENTRY !!!! | | UNCLASSIFIED | 1003 |
| 2970 | 71777223 (9441, 9442) | Novel Protein sim. GBank g 113671 sp P23964 ALUE_HUMAN - !!! ALU CLASS F WARNING ENTRY !!!! | | UNCLASSIFIED | 1024, 1039 |
| 2971 | 10886338 (16999, 17000) | Novel Protein sim. GBank g 114009 sp P05636 APAG_ECOLI - APAG PROTEIN | | UNCLASSIFIED | 1027 |

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| 2972 | 79617144 (2693, 2694) | Novel Protein sim. GBank gj 114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT) | | UNCLASSIFIED | 1034 |
| 2973 | 20715326 (21353, 21354) | Novel Protein sim. GBank gj 114157 sp P22675 ARLY_CHLRE - ARGININOSUCCINATE LYASE (ARGINOSUCCINASE) (ASAL) | | UNCLASSIFIED | 1022 |
| 2974 | 78765614 (9833, 9834) | Novel Protein sim. GBank gj 1143538 emb CAA61138 - (X87883) mitochondrial capsule selenoprotein [Rattus norvegicus] | | UNCLASSIFIED | 1023, 1039 |
| 2975 | 80058750 (12813, 12814) | Novel Protein sim. GBank gj 1146192 (L47838) - putative [Bacillus subtilis] | | UNCLASSIFIED | 1010 |
| 2976 | 79568002 (7401, 7402) | Novel Protein sim. GBank gj 114878 sp P11435 BCPA_STRHY - CARBOXYVINYLCARBOXYPHOSPHONATE PHOSPHORYLMUTASE (CARBOXYPHOSPHONOENOLPYRUVATE PHOSPHONOMUTASE) (CPEP PHOSPHONOMUTASE) | | UNCLASSIFIED | 1044 |
| 2977 | 94669043 (20705, 20706) | Novel Protein sim. GBank gj 1150834 (U42471) - Wiscott-Aldrich Syndrome protein homolog [Mus musculus] | | UNCLASSIFIED | 1022, 1024 |
| 2978 | 17884320 (17465, 17466) | Novel Protein sim. GBank gj 115160 sp P26762 BVGS_BORBR - VIRULENCE SENSOR PROTEIN BVGS PRECURSOR | | UNCLASSIFIED | 1039 |
| 2979 | 9856934 (7951, 7952) | Novel Protein sim. GBank gj 115284 sp CA12_BOVIN_1 - [Segment 1 of 2] COLLAGEN ALPHA 1(II) CHAIN | | UNCLASSIFIED | 1008 |
| 2980 | 13517321 (5119, 5120) | Novel Protein sim. GBank gj 1155068 emb CAA644425 - (X94976) cell wall-plasma membrane linker protein [Brassica napus] | | UNCLASSIFIED | 1024 |
| 2981 | 80026320 (5637, 5638) | Novel Protein sim. GBank gj 115953 sp P25342 CC10_YEAST - CELL DIVISION CONTROL PROTEIN 10 | | UNCLASSIFIED | 1004 |

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| 2982 | 20281932 (10945, 10946) | Novel Protein sim. GBank gil160355 (U33058) - UNC-89 [Caenorhabditis elegans] | UNCLASSIFIED | 1022 |
| 2983 | 80254017 (4609, 4610) | Novel Protein sim. GBank gil1166450 lemb CAA645591 - (X95262) Tfml | UNCLASSIFIED | 1004, 1006, 1008, 1016, 1017, 1023, 1024 |
| 2984 | 78675362 (20027, 20028) | Novel Protein sim. GBank gil116701 sp P05481 HEAD_BPPH8 - MAJOR HEAD PROTEIN (GPE) (GP5) (MAJOR COAT PROTEIN) | UNCLASSIFIED | 1008 |
| 2985 | 10147068 (8803, 8804) | Novel Protein sim. GBank gil1167955 (U43497) - putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare] | UNCLASSIFIED | 1054 |
| 2986 | 12840694 (11339, 11340) | Novel Protein sim. GBank gil1168224 sp P4456915NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR | UNCLASSIFIED | 1022 |
| 2987 | 66149064 (8003, 8004) | Novel Protein sim. GBank gil1168373 sp P46815 AG84_MYCLE - ANTIGEN 84 | UNCLASSIFIED | 1003 |
| 2988 | 29459741 (8699, 8700) | Novel Protein sim. GBank gil1168816 sp P30665 CC54_YEAST - CELL DIVISION CONTROL PROTEIN 54 | UNCLASSIFIED | 1026 |
| 2989 | 78747885 (16909, 16910) | Novel Protein sim. GBank gil1169207 sp P21705 DA82_YEAST - DAL82 PROTEIN | UNCLASSIFIED | 1022 |
| 2990 | 13086022 (2419, 2420) | Novel Protein sim. GBank gil1169224 sp P44514 DAPE_HAEIN - SUCINYL DIAMINOPIMELATE DESUCCINYLASE (SDAP) | UNCLASSIFIED | 1022 |
| 2991 | 20438284 (14597, 14598) | Novel Protein sim. GBank gil1169268 sp P44430 DEOC_HAEIN - DEOXYRIBOSE-PHOSPHATE ALDOLASE (PHOSPHODEOXYRIBOALDOLASE) (DEOXYRIBOALDOLASE) | UNCLASSIFIED | 1010 |
| 2992 | 20466524 (9123, 9124) | Novel Protein sim. GBank gil1169479 sp P43925IEFG_HAEIN - ELONGATION FACTOR G (EF-G) | UNCLASSIFIED | 1010 |

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| 2993 3140) | 19858781 (3139, Novel Protein sim. GBank g 1169692 sp P41813 FKH2_YEAST - FORK HEAD PROTEIN HOMOLOG 2 | | UNCLASSIFIED | 1022 |
| 2994 21516) | 79618456 (21516), Novel Protein sim. GBank g 1169692 sp P41813 FKH2_YEAST - FORK HEAD PROTEIN HOMOLOG 2 | | UNCLASSIFIED | 1008 |
| 2995 17356) | 35365320 (17355, Novel Protein sim. GBank g 1169748 sp P43500 FRZC_NYXXA - FRZCD PROTEIN (FRIZZY AGGREGATION PROTEIN FRZCD) | | UNCLASSIFIED | 1050 |
| 2996 12244) | 11083699 (12243, Novel Protein sim. GBank g 1169821 sp P13227 GAL1_STRL1 - GALACTOKINASE | | UNCLASSIFIED | 1024 |
| 2997 15078) | 11688227 (15077, Novel Protein sim. GBank g 1170243 sp P43413 HEMZ_YEREN - FERROCHELATASE (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) | | UNCLASSIFIED | 1008 |
| 2998 12666) | 20465707 (12665, Novel Protein sim. GBank g 1170440 sp P44523 HXC1_HAEIN - HEME- HEMOPEXIN UTILIZATION PROTEIN C PRECURSOR | | UNCLASSIFIED | 1010 |
| 2999 12614) | 30251531 (12613), Novel Protein sim. GBank g 1170490 sp P46989 IDS2_YEAST - IME2- DEPENDENT SIGNALING PROTEIN | | UNCLASSIFIED | 1026 |
| 3000 19236) | 21424644 (19235), Novel Protein sim. GBank g 1170490 sp P46989 IDS2_YEAST - IME2- DEPENDENT SIGNALING PROTEIN | | UNCLASSIFIED | 1022 |
| 3001 18634) | 80249807 (18633), Novel Protein sim. GBank g 1170500 sp P44323 F2_HAEIN - TRANSLATION INITIATION FACTOR IF-2 | | UNCLASSIFIED | 1034 |
| 3002 5858) | 79840765 (5857, Novel Protein sim. GBank g 1170546 sp P44851 LVD_HAEIN - DIHYDROXY-ACID DEHYDRATASE (DAD) | | UNCLASSIFIED | 1022, 1024, 1034 |
| 3003 66151504 (669, 670) | 66151504 (669, Novel Protein sim. GBank g 1170593 sp P14542 UTA_ECOLI - FERRIC AEROBACTIN RECEPTOR PRECURSOR (CLOACIN RECEPTOR) | | UNCLASSIFIED | 1024 |

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| 3004 | 16838677 (17495, 17496) | Novel Protein sim. GBank gi 1170923 sp P44566 MEPA_HAEIN - PENICILLIN-INSENSITIVE MUREIN - ENDOPEPTIDASE PRECURSOR | | UNCLASSIFIED | 1039 |
| 3005 | 20724429 (15081, 15082) | Novel Protein sim. GBank gi 1170933 sp P45331 METE_HAEIN - 5'- METHYLTRIHYDROPTEROYL TRIGLUTAMATE-- HOMOCYSTEINE METHYL TRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN- INDEPENDENT METHIONINE SYNTHASE) | | UNCLASSIFIED | 1006 |
| 3006 | 80219473 (5967, 5968) | Novel Protein sim. GBank gi 1170950 sp P43638 MHP1_YEAST - MAP- HOMOLOGOUS PROTEIN 1 | | UNCLASSIFIED | 1003, 1004, 1006, 1010, 1022, 1024, 1026, 1034 |
| 3007 | 80468156 (8967, 8968) | Novel Protein sim. GBank gi 1171071 sp P45066 MURC_HAEIN - UDP-N- ACETYL MURAMATE--ALANINE LIGASE (UDP-N- ACETYL MURANOYL-L-ALANINE SYNTHETASE) | | UNCLASSIFIED | 1012 |
| 3008 | 11077849 (11309, 11310) | Novel Protein sim. GBank gi 1172222 (U44834) - polyphosphate glucokinase [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1024 |
| 3009 | 79961872 (13373, 13374) | Novel Protein sim. GBank gi 1172541 sp P47190 PMT3_YEAST - DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSEYLTRANSFERASE 3 | | UNCLASSIFIED | 1006, 1010, 1023, 1024, 1034 |
| 3010 | 16843342 (21013, 21014) | Novel Protein sim. GBank gi 1172543 sp P42934 PMT6_YEAST - DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSEYLTRANSFERASE 6 | | UNCLASSIFIED | 1023 |

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| 3011 | 52388083 (2143, 2144) | Novel Protein sim. GBank gi 1172548 sp P43010 PNTB_HAEIN - NAD(P) TRANSHYDROGENASE SUBUNIT BETA (PYRIDINE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA) (NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA) | UNCLASSIFIED | 1036 |
| 3012 | 80060010 (16911, 16912) | Novel Protein sim. GBank gi 1172548 sp P43010 PNTB_HAEIN - NAD(P) TRANSHYDROGENASE SUBUNIT BETA (PYRIDINE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA) (NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA) | UNCLASSIFIED | 1008, 1010, 1034 |
| 3013 | 19641642 (2853, 2854) | Novel Protein sim. GBank gi 1172617 sp P44647 PRIA_HAEIN - PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) | UNCLASSIFIED | 1004 |
| 3014 | 80502022 (14297, 14298) | Novel Protein sim. GBank gi 1172803 sp P43123 QRI1_YEAST - HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION | UNCLASSIFIED | 1001, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1026, 1027, 1034, 1038, 1039, 1044 |
| 3015 | 38915945 (10801, 10802) | Novel Protein sim. GBank gi 1174092 (U43360) - reverse transcriptase [Peromyscus maniculatus] | UNCLASSIFIED | 1026 |
| 3016 | 65668295 (22243, 22244) | Novel Protein sim. GBank gi 1174503 sp P43817 SYD_HAEIN - ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) | UNCLASSIFIED | 1016 |
| 3017 | 25260301 (4541, 4542) | Novel Protein sim. GBank gi 1174549 sp P43834 SYV_HAEIN - VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) | UNCLASSIFIED | 1008 |

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| 3018 | 30503862 (705, 706) | Novel Protein sim. GBank gi 1174661 sp P4454 TGT_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) | UNCLASSIFIED | 1009 |
| 3019 | 78795379 (3317, 3318) | Novel Protein sim. GBank gi 1174933 sp P44907 VACB_HAEIN - VACB PROTEIN HOMOLOG | UNCLASSIFIED | 1026 |
| 3020 | 78757424 (9923, 9924) | Novel Protein sim. GBank gi 1174933 sp P44907 VACB_HAEIN - VACB PROTEIN HOMOLOG | UNCLASSIFIED | 1030 |
| 3021 | 17902237 (16721, 16722) | Novel Protein sim. GBank gi 1175715 sp P41479 Y091_NPVAC - HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION | UNCLASSIFIED | 1044 |
| 3022 | 11070511 (18511, 18512) | Novel Protein sim. GBank gi 1175173 sp P43954 Y152_HAEIN - HYPOTHETICAL PROTEIN_H 0152 | UNCLASSIFIED | 1008 |
| 3023 | 20436667 (15399, 15400) | Novel Protein sim. GBank gi 1175322 sp P44917 Y883_HAEIN - HYPOTHETICAL PROTEIN_H 0883 | UNCLASSIFIED | 1010 |
| 3024 | 80221613 (7483, 7484) | Novel Protein sim. GBank gi 1175395 sp Q09723 YA42_SCHPO - HYPOTHETICAL 14.1 KD PROTEIN C31A2.02 IN CHROMOSOME 1 | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1024, 1026, 1034 |
| 3025 | 11093343 (4863, 4864) | Novel Protein sim. GBank gi 1175512 sp P39717 YA56_YEAST - HYPOTHETICAL 95.1 KD PROTEIN IN CNE1 ACS1 INTERGENIC REGION | UNCLASSIFIED | 1022 |
| 3026 | 16425308 (8001, 8002) | Novel Protein sim. GBank gi 1175641 sp P44720 YCCEG_HAEIN - HYPOTHETICAL PROTEIN_H 0457 | UNCLASSIFIED | 1017 |
| 3027 | 78917082 (22569, 22570) | Novel Protein sim. GBank gi 1175652 sp P44551 TRMU_HAEIN - PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE | UNCLASSIFIED | 1039 |

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| 3028 | 27346644 (16079, 16080) | Novel Protein sim. GBank gi 1175653 sp P44736 YCFC_HAEIN - HYPOTHETICAL PROTEIN H10638 | | UNCLASSIFIED | 1022 |
| 3029 | 20724165 (16651, 16652) | Novel Protein sim. GBank gi 1175655 sp P44683 YCFD_HAEIN - HYPOTHETICAL PROTEIN H10396 | | UNCLASSIFIED | 1006 |
| 3030 | 85680835 (16085, 16086) | Novel Protein sim. GBank gi 1175866 sp P44227 YF05_HAEIN - HYPOTHETICAL PROTEIN H11505 | | UNCLASSIFIED | 1001, 1031, 1038 |
| 3031 | 11608969 (3233, 3234) | Novel Protein sim. GBank gi 1175927 sp P43578 YFB5_YEAST - HYPOTHETICAL 19.3 KD PROTEIN IN MDJ1- HSP12 INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 3032 | 80079333 (3815, 3816) | Novel Protein sim. GBank gi 1175986 sp P43585 YF12_YEAST - HYPOTHETICAL 22.4 KD PROTEIN IN GCN20- CMK1 INTERGENIC REGION PRECURSOR | | UNCLASSIFIED | 1006, 1017, 1034, 1039 |
| 3033 | 80546722 (12225, 12226) | Novel Protein sim. GBank gi 1175990 sp P43598 YF17_YEAST - HYPOTHETICAL 21.8 KD PROTEIN IN UGS1- FAB1 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1004, 1006, 1008, 1010, 1022, 1023, 1024, 1027, 1031, 1034, 1058 |
| 3034 | 80503206 (14003, 14004) | Novel Protein sim. GBank gi 1176023 sp P43618 YFL6_YEAST - HYPOTHETICAL 41.3 KD PROTEIN IN SAP155- YMR31 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1012, 1017, 1022, 1024, 1034, 1044, 1054 |
| 3035 | 57293445 (7473, 7474) | Novel Protein sim. GBank gi 1176026 sp P43621 COPD_YEAST - COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) | | UNCLASSIFIED | 1022, 1034 |
| 3036 | 87462658 (13775, 13776) | Novel Protein sim. GBank gi 1176160 sp P42628 YHAM_ECOLI - HYPOTHETICAL 19.4 KD PROTEIN IN EXUR- TDCC INTERGENIC REGION (F188) | | UNCLASSIFIED | 1004, 1006, 1010, 1015, 1016, 1024 |

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| 3037 | 77520579 (16077, 16078) | Novel Protein sim. GBank g 1176261 sp P5804 YHGE_ECOLI - HYPOTHETICAL 64.6 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION (F574) | UNCLASSIFIED | 1049 |
| 3038 | 79835018 (5813, 5814) | Novel Protein sim. GBank g 1176281 sp P46852 YHHW_ECOLI - HYPOTHETICAL 26.3 KD PROTEIN IN GNTR-GGT INTERGENIC REGION (F231) | UNCLASSIFIED | 1008 |
| 3039 | 80412661 (6701, 6702) | Novel Protein sim. GBank g 1176481 sp P39408 YJUV_ECOLI - HYPOTHETICAL 28.9 KD PROTEIN IN OSMY-DEOC INTERGENIC REGION | UNCLASSIFIED | 1029 |
| 3040 | 78741833 (18065, 18066) | Novel Protein sim. GBank g 1176587 sp P42843 YN51_YEAST - HYPOTHETICAL 88.9 KD PROTEIN IN RFA2-STB1 INTERGENIC REGION | UNCLASSIFIED | 1008 |
| 3041 | 823337545 (22717, 22718) | Novel Protein sim. GBank g 1176589 sp P42845 STB1_YEAST - STB1 PROTEIN | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1027, 1031, 1034, 1038, 1039, 1044 |
| 3042 | 35933693 (13009, 13010) | Novel Protein sim. GBank g 1176071 sp P45637 YPR_A_CORGL - HYPOTHETICAL 33.0 KD PROTEIN IN PROA-PROA INTERGENIC REGION | UNCLASSIFIED | 1053 |
| 3043 | 78675448 (521, 522) | Novel Protein sim. GBank g 1176918 sp P24089 YSY2_YEAST - HYPOTHETICAL 137.7 KD PROTEIN IN SUBTELOMERIC Y' REPEAT REGION OF CHR XV (ORF 2) | UNCLASSIFIED | 1022 |
| 3044 | 25316869 (15795, 15796) | Novel Protein sim. GBank g 11769861 sp P42413 OLB_BACSU - IOLB PROTEIN | UNCLASSIFIED | 1008 |

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| 3045 | 78786773 (5179, 5180) | Novel Protein sim. GBank gil1177607 emb CAA6321 9] - (X92485) pva1 [Plasmidium vivax] | | UNCLASSIFIED | 1044 |
| 3046 | 20466944 (20991, 20992) | Novel Protein sim. GBank gil118244 sp P24176 DAPE_ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (SDAP) | | UNCLASSIFIED | 1010 |
| 3047 | 20729206 (8609, 8610) | Novel Protein sim. GBank gil118248 sp P13483 DATI_YEAST - OLIGO(A)YOLIGO(T)-BINDING PROTEIN (DATIN) | | UNCLASSIFIED | 1010 |
| 3048 | 30001150 (8871, 8872) | Novel Protein sim. GBank gil118412 sp P09548 DEDA_ECOLI - DEDA PROTEIN (DSG-1 PROTEIN) | | UNCLASSIFIED | 1030 |
| 3049 | 12969395 (7621, 7622) | Novel Protein sim. GBank gil1184121 (U20808) - auxin-induced protein [Vigna radiata] | | UNCLASSIFIED | 1024 |
| 3050 | 78789040 (10609, 10610) | Novel Protein sim. GBank gil119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN | | UNCLASSIFIED | 1008 |
| 3051 | 32545225 (6651, 6652) | Novel Protein sim. GBank gil119111 sp P12978 EBN2_EBV - EBNA-2 NUCLEAR PROTEIN | | UNCLASSIFIED | 1023 |
| 3052 | 80248724 (16629, 16630) | Novel Protein sim. GBank gil1195494 bb s1170178, Pax-1 product=scriftoome development regulator/DNA-binding transcriptional activator [Coturnix coturnix=Japanese quail, ssp. japonica, Peptid, 353 aa] | | UNCLASSIFIED | 1053 |
| 3053 | 80225738 (16205, 16206) | Novel Protein sim. GBank gil1196398 (M21305) - unknown protein [Homo sapiens] | | UNCLASSIFIED | 1053 |
| 3054 | 9282925 (7381, 7382) | Novel Protein sim. GBank gil1196743 (M14365) - unknown protein [Pseudomonas syringae] | | UNCLASSIFIED | 1003 |
| 3055 | 65681679 (19121, 19122) | Novel Protein sim. GBank gil119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) | | UNCLASSIFIED | 1046 |

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| 3056 | 37811605 (22153, 22154), | Novel Protein sim. GBank gi 119328 sp P27787 FER1_MAIZE - FERREDOXIN I PRECURSOR (FD_I) | | UNCLASSIFIED | 1058 |
| 3057 | 80430917 (22633, 22634) | Novel Protein sim. GBank gi 1193536 emb CAA64900 - (X95644) ORF 2310 [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1006, 1038 |
| 3058 | 82101992 (15149, 15150) | Novel Protein sim. GBank gi 120304 sp P13932 FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1) | | UNCLASSIFIED | 1016, 1024 |
| 3059 | 79628254 (12803, 12804) | Novel Protein sim. GBank gi 120393 sp P13421 IFMA_SERMFA - FIMBRIA A PROTEIN PRECURSOR | | UNCLASSIFIED | 1039 |
| 3060 | 79231403 (7845, 7846) | Novel Protein sim. GBank gi 121058 sp P127554 E2BD_YEAST - TRANSLATION INITIATION FACTOR EIF-2B DELTA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTORY) (GUANINE NUCLEOTIDE EXCHANGE FACTORY SUBUNIT GCD2) (GCD COMPLEX SUBUNIT GCD2) | | UNCLASSIFIED | 1001, 1017 |
| 3061 | 87896252 (687, 688) | Novel Protein sim. GBank gi 1213021 emb CAA59198 - (X84710) ORF492, surface antigen gene [Methanoscarcina mazei] | | UNCLASSIFIED | 1015 |
| 3062 | 78949714 (7795, 7796) | Novel Protein sim. GBank gi 121644 sp P7816 GRP_HORVU - GLYCINE- RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR | | UNCLASSIFIED | 1023 |
| 3063 | 85518675 (22333, 22334) | Novel Protein sim. GBank gi 121893 sp P13364 GYRB_PSEPU - DNA GYRASE SUBUNIT B | | UNCLASSIFIED | 1049 |
| 3064 | 70949771 (20929, 20930) | Novel Protein sim. GBank gi 123153 sp P16249 HISS5_STRCO - AMIDOTRANSFERASE HISCH | | UNCLASSIFIED | 1029 |

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| 3065 | 47666134 (17539, 17540) | Novel Protein sim. GBank gi 1234787 (U37373) - up-regulated by thyroid hormone in tadpoles; expressed specifically in the tail and only at metamorphosis; membrane bound or extracellular protein; C-terminal basic region [Xenopus laevis] | UNCLASSIFIED | 1040 |
| 3066 | 20375525 (6805, 6806) | Novel Protein sim. GBank gi 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1010 |
| 3067 | 20717335 (20081, 20082) | Novel Protein sim. GBank gi 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1034 |
| 3068 | 91213832 (13991, 13992) | Novel Protein sim. GBank gi 1235974 emb CAA65474 - (X96713) collagen [Globodera pallida] | UNCLASSIFIED | 1016, 1024 |
| 3069 | 15023758 (3185, 3186) | Novel Protein sim. GBank gi 1236781 emb CAA65507 - (X96732) cuticular collagen [Ostertagia circumciscta] | UNCLASSIFIED | 1001 |
| 3070 | 80504151 (6465, 6466) | Novel Protein sim. GBank gi 125329 sp P0495 KDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS) | UNCLASSIFIED | 1012 |
| 3071 | 11245720 (9245, 9246) | Novel Protein sim. GBank gi 125963 sp P11048 LAMA_XENLA - LAMIN A | UNCLASSIFIED | 1010 |
| 3072 | 57301013 (357, 358) | Novel Protein sim. GBank gi 126215 sp P13838 LEUK_RAT - LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIALOPHORIN) (CD43) (W3/13 ANTIGEN) | UNCLASSIFIED | 1006, 1029, 1034, 1044 |
| 3073 | 28392794 (22241, 22242) | Novel Protein sim. GBank gi 1262369 emb CAA94716 - (Z70722) hypothetical protein [Mycobacterium leprae] | UNCLASSIFIED | 1044 |

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| 3074 12742) | 70942037 (12741, Novel Protein sim. GBank gi 126295 sp P08547 LIN1_HUMAN - LINE-1 REVERSE TRANSCRIPTASE HOMOLOG | | UNCLASSIFIED | 1024 |
| 3075 13502) | 78462796 (13501, Novel Protein sim. GBank gi 126296 sp P08548 LIN1_NYCCO - LINE-1 REVERSE TRANSCRIPTASE HOMOLOG | | UNCLASSIFIED | 1026 |
| 3076 79247392 (1213, 1214) | Novel Protein sim. GBank gi 126654 sp P03030 LYSR_ECOLI - TRANSCRIPTIONAL ACTIVATOR PROTEIN LYSR | | UNCLASSIFIED | 1039 |
| 3077 12154) | Novel Protein sim. GBank gi 126725 sp P21139 MAN1_RAT - ALPHA- MANNOSIDASE (ALPHA-D-MANNOSIDE MANNOHYDROLASE) | | UNCLASSIFIED | 1006, 1022 |
| 3078 82125916 (9133, 9134) | Novel Protein sim. GBank gi 127028 sp P15807 MET8_YEAST - MET8 PROTEIN | | UNCLASSIFIED | 1004, 1006, 1012, 1016, 1022, 1024, 1025, 1026, 1034, 1039 |
| 3079 19052) | Novel Protein sim. GBank gi 127114 sp P23060 MK32_YEAST - MAK32 PROTEIN | | UNCLASSIFIED | 1026 |
| 3080 17260) | 20212392 (17259, 17260) | Novel Protein sim. GBank gi 1272368 (U51896) - LfgE (<i>Vibrio parahaemolyticus</i>) | UNCLASSIFIED | 1010 |
| 3081 82437397 (2193, 2194) | Novel Protein sim. GBank gi 127550 sp P11653 MUTB_PROF-R - METHYLMALONYL-COA MUTASE ALPHA- SUBUNIT (MCM-ALPHA) | | UNCLASSIFIED | 1001, 1004, 1010, 1012, 1022, 1027, 1034, 1038, 1049 |
| 3082 19742) | 57300594 (19741, 19742) | Novel Protein sim. GBank gi 1293563 (U49188) - Dif33 gene product [<i>Homo sapiens</i>] | UNCLASSIFIED | 1010, 1022 |
| 3083 20608418 (1011, 1012) | Novel Protein sim. GBank gi 128541 sp P15558 PAC2_PSESS3 - PENICILLIN ACYLASE II PRECURSOR (PENICILLIN AMIDASE II) (CEPHALOSPORIN ACYLASE II) | | UNCLASSIFIED | 1004 |

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| 3084 | 20724611 (14715, 14716) | Novel Protein sim. GBank g 129670 sp P02981 PBPA_ECOLI - PENICILLIN-BINDING PROTEIN 1A (PBP-1A) | | UNCLASSIFIED | 1006 |
| 3085 | 79607900 (20537, 20538) | Novel Protein sim. GBank g 129828 sp P24328 PERT_BORPA - PERTACTIN PRECURSOR (OUTER MEMBRANE PROTEIN P.70) (P.95) | | UNCLASSIFIED | 1034 |
| 3086 | 78992963 (13165, 13166) | Novel Protein sim. GBank g 130776 sp P20006 PPLA_RABIT - CARDIAC PHOSPHOLAMBAN (PLB) | | UNCLASSIFIED | 1008 |
| 3087 | 20292941 (3973, 3974) | Novel Protein sim. GBank g 130999 sp P05142 PRP2_MOUSE - PROLINE-RICH PROTEIN MP-2 PRECURSOR | | UNCLASSIFIED | 1034 |
| 3088 | 6757112 (6181, 8182) | Novel Protein sim. GBank g 131000 sp P10164 PRP2_RAT - ACIDIC PROLINE-RICH PROTEIN PRP25 (CLONE PRP25) | | UNCLASSIFIED | 1022 |
| 3089 | 80216614 (7201, 7202) | Novel Protein sim. GBank g 131002 sp P05143 PRP3_MOUSE - PROLINE-RICH PROTEIN MP-3 | | UNCLASSIFIED | 1009, 1024, 1031 |
| 3090 | 20290873 (17893, 17894) | Novel Protein sim. GBank g 1314732 U54640 - 185 kDa silk protein [Chironomus pallidivittatus] | | UNCLASSIFIED | 1034 |
| 3091 | 78758266 (18971, 18972) | Novel Protein sim. GBank g 131653 sp P25502 PUT3_YEAST - PROLINE UTILIZATION TRANS-ACTIVATOR | | UNCLASSIFIED | 1039, 1044, 1054 |
| 3092 | 57303110 (18523, 18524) | Novel Protein sim. GBank g 132339 sp P03872 REP2_YEAST - TRANS-ACTING FACTOR C (REP2) (PROTEIN CHARLIE) | | UNCLASSIFIED | 1004, 1022, 1026, 1034, 1039 |
| 3093 | 79568236 (5679, 5680) | Novel Protein sim. GBank g 132360 sp P05684 REPC_AGRRA - POSSIBLE REPLICATION PROTEIN C | | UNCLASSIFIED | 1008 |

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| 3094 | 78755150 (3441, 3442) | Novel Protein sim. GBank gi 1325621 sp P25235 RIB2_RAT - DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOSYLTRANSFERASE 63 KD SUBUNIT PRECURSOR (RIBOPHORIN II) | | UNCLASSIFIED | 1009 |
| 3095 | 36622940 (8273, 8274) | Novel Protein sim. GBank gi 1326381 (U58751) - coded by C. elegans cDNA yk9hs.5; coded for by C. elegans cDNA yk9hs5.3; coded for by C. elegans cDNA CEESH72F; coded for by C. elegans cDNA CEESB62F; coded for by C. elegans cDNA yk110g2.3; coded for by C. elegans cDNA yk110g2.5... | | UNCLASSIFIED | 1034 |
| 3096 | 65657000 (9415, 9416) | Novel Protein sim. GBank gi 1335199 emb CAA26919 - (X03145) pot. ORF V [Homo sapiens] | | UNCLASSIFIED | 1054 |
| 3097 | 10173056 (231, 232) | Novel Protein sim. GBank gi 1335205 emb CAA36480 - (X52235) ORFII [Homo sapiens] | | UNCLASSIFIED | 1001 |
| 3098 | 33188734 (8665, 8666) | Novel Protein sim. GBank gi 1335205 emb CAA36480 - (X52235) ORFII [Homo sapiens] | | UNCLASSIFIED | 1026 |
| 3099 | 80077692 (2217, 2218) | Novel Protein sim. GBank gi 134319 sp P07819 SCRB_BACSU - SUCROSE-6-PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE) | | UNCLASSIFIED | 1034 |
| 3100 | 37001319 (1769, 1770) | Novel Protein sim. GBank gi 1343389 sp P15040 SECB_ECOLI - PROTEIN EXPORT PROTEIN SECB | | UNCLASSIFIED | 1001 |
| 3101 | 9883571 (14501, 14502) | Novel Protein sim. GBank gi 134400 sp P16920 SECE_ECOLI - PREPROTEIN TRANSLOCASE SECE SUBUNIT | | UNCLASSIFIED | 1008 |
| 3102 | 17950910 (557, 558) | Novel Protein sim. GBank gi 1346563 sp P49308 MOCB_RHIME - PUTATIVE RHIZOPINE-BINDING PROTEIN PRECURSOR | | UNCLASSIFIED | 1054 |

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| 3103 | 78363353 (8369, 8370) | Novel Protein sim. GBank gi 1346647 sp P49687 N145_YEAST - NUCLEOPORIN NUP145 (NUCLEAR PORE PROTEIN NUP145) | | UNCLASSIFIED | 1003 |
| 3104 | 11310751 (19601, 19602) | Novel Protein sim. GBank gi 1346886 sp P25270 PT56_YEAST - RIBOSE METHYLTRANSFERASE PET56 (MITOCHONDRIAL LARGE RIBOSOMAL RNA RIBOSE METHYLASE) (21S rRNA [GM225] 2' O METHYLTRANSFERASE) | | UNCLASSIFIED | 1022 |
| 3105 | 39432508 (19695, 19696) | Novel Protein sim. GBank gi 1346886 sp P25270 PT56_YEAST - RIBOSE METHYLTRANSFERASE PET56 (MITOCHONDRIAL LARGE RIBOSOMAL RNA RIBOSE METHYLASE) (21S rRNA [GM225] 2' O METHYLTRANSFERASE) | | UNCLASSIFIED | 1006 |
| 3106 | 80240870 (10127, 10128) | Novel Protein sim. GBank gi 1346910 sp P28650 PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP-ASPARTATE LIGASE) | | UNCLASSIFIED | 1022 |
| 3107 | 79873033 (12885, 12886) | Novel Protein sim. GBank gi 134752 sp P17122 SP16_YEAST - SPORULATION PROTEIN SPO16 | | UNCLASSIFIED | 1001, 1006, 1022 |
| 3108 | 79910699 (16435, 16436) | Novel Protein sim. GBank gi 134856 sp P09139 SPYA_RAT - SERINE - PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (SPT) (ALANINE--GLYOXYLATE AMINOTRANSFERASE) (AGT) | | UNCLASSIFIED | 1023 |
| 3109 | 27843819 (4371, 4372) | Novel Protein sim. GBank gi 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185) | | UNCLASSIFIED | 1034 |

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| 3110 | 11017734 (4395, 4396) | Novel Protein sim. GBank gi 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185) | UNCLASSIFIED | 1001 |
| 3111 | 80032445 (16297, 16298) | Novel Protein sim. GBank gi 134935 sp P11972 SST2_YEAST - SST2 PROTEIN | UNCLASSIFIED | 1001, 1004, 1006, 1008, 1022 |
| 3112 | 78789044 (11047, 11048) | Novel Protein sim. GBank gi 1351823 sp P48238 YG3O_YEAST - HYPOTHETICAL 25.2 KD PROTEIN IN RSR1-CYS4 INTERGENIC REGION | UNCLASSIFIED | 1003, 1026 |
| 3113 | 78473387 (18227, 18228) | Novel Protein sim. GBank gi 135192 sp P22326 SYY1_BACSU - TYROSYL-TRNA SYNTHETASE 1 (TYROSINE--TRNA LIGASE) (TYRS 1) | UNCLASSIFIED | 1026 |
| 3114 | 9274026 (15995, 15996) | Novel Protein sim. GBank gi 1352123 sp P21637 COBG_PSEDE - COBG PROTEIN | UNCLASSIFIED | 1004 |
| 3115 | 78916113 (4179, 4180) | Novel Protein sim. GBank gi 1352209 sp P32225 DBF4_YEAST - DBF4 PROTEIN (DNA52 PROTEIN) | UNCLASSIFIED | 1022, 1039 |
| 3116 | 80053089 (1671, 1672) | Novel Protein sim. GBank gi 1352429 sp P02995 IF2_ECOLI - TRANSLATION INITIATION FACTOR IF-2 | UNCLASSIFIED | 1004 |
| 3117 | 78726661 (18631, 18632) | Novel Protein sim. GBank gi 1352955 sp P47076 YJB1_YEAST - HYPOTHETICAL 18.6 KD PROTEIN IN CCT3-CCT8 INTERGENIC REGION | UNCLASSIFIED | 1022, 1026 |
| 3118 | 57292988 (14891, 14892) | Novel Protein sim. GBank gi 1352961 sp P47070 YJB8_YEAST - HYPOTHETICAL 11.7 KD PROTEIN IN PET130-CCT3 INTERGENIC REGION | UNCLASSIFIED | 1004, 1006, 1010, 1024, 1034 |
| 3119 | 27848737 (17097, 17098) | Novel Protein sim. GBank gi 1352961 sp P47063 YJC7_YEAST - HYPOTHETICAL 15.7 KD PROTEIN IN MAD2-RNR2 INTERGENIC REGION | UNCLASSIFIED | 1022, 1024, 1034 |

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| 3120 | 27366151 (9787, 9788) | Novel Protein sim. G-Bank gi 1353033 sp P46933 YJR0_YEAST - HYPOTHETICAL 22.0 KD PROTEIN IN CPS1-FPP1 INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 3121 | 57302037 (21081, 21082) | Novel Protein sim. G-Bank gi 1353033 sp P46933 YJR0_YEAST - HYPOTHETICAL 22.0 KD PROTEIN IN CPS1-FPP1 INTERGENIC REGION | | UNCLASSIFIED | 1008, 1034 |
| 3122 | 78938103 (10325, 10326) | Novel Protein sim. G-Bank gi 1353046 sp P47082 YJX1_YEAST - HYPOTHETICAL 65.3 KD PROTEIN IN PRE3-SAG1 INTERGENIC REGION | | UNCLASSIFIED | 1017 |
| 3123 | 78948525 (22561, 22562) | Novel Protein sim. G-Bank gi 1353108 sp P48566 YN33_YEAST - HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION | | UNCLASSIFIED | 1017, 1022, 1023 |
| 3124 | 17294765 (1945, 1946) | Novel Protein sim. G-Bank gi 1353221 sp P13390 VLTF_BT5 - L-SHAPED TAIL FIBRE PROTEIN (LTF PROTEIN) | | UNCLASSIFIED | 1039 |
| 3125 | 16778371 (5223, 5224) | Novel Protein sim. G-Bank gi 1353537 (U38906) - dUTPase [Bacteriophage r1] | | UNCLASSIFIED | 1044 |
| 3126 | 79769235 (9779, 9780) | Novel Protein sim. G-Bank gi 135514 sp P06333 TCB1_RAB1 - T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11) | | UNCLASSIFIED | 1017 |
| 3127 | 80500474 (20245, 20246) | Novel Protein sim. G-Bank gi 1357001 sp P19675 TGT_ECOLI - QUEINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) | | UNCLASSIFIED | 1012 |
| 3128 | 56007249 (21497, 21498) | Novel Protein sim. G-Bank gi 135914 sp P17408 TLM_MOUSE - TLM PROTEIN(TLM ONCOGENE) | | UNCLASSIFIED | 1019 |
| 3129 | 78385457 (6405, 6406) | Novel Protein sim. G-Bank gi 1361057 pir IS6582 - hypothetical protein f192 - Escherichia coli | | UNCLASSIFIED | 1026 |

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| 3130 | 85518635 (14423) 14424) | Novel Protein sim. GBank gi 1361153 pir S58602 - hypothetical protein o211 - Escherichia coli | | UNCLASSIFIED | 1049 |
| 3131 | 27981297 (15969, 15970) | Novel Protein sim. GBank gi 136141 sp P19774 TRA9_MYCTU - PUTATIVE TRANSPOSEASE FOR INSERTION SEQUENCE ELEMENT IS986 (ORFB) | | UNCLASSIFIED | 1006 |
| 3132 | 11764353 (17809, 17810) | Novel Protein sim. GBank gi 136141 sp P19774 TRA9_MYCTU - PUTATIVE TRANSPOSEASE FOR INSERTION SEQUENCE ELEMENT IS986 (ORFB) | | UNCLASSIFIED | 1022 |
| 3133 | 37034111 (21619, 21620) | Novel Protein sim. GBank gi 136141 sp P19774 TRA9_MYCTU - PUTATIVE TRANSPOSEASE FOR INSERTION SEQUENCE ELEMENT IS986 (ORFB) | | UNCLASSIFIED | 1012 |
| 3134 | 24128986 (17695, 17696) | Novel Protein sim. GBank gi 1362491 pir S58652 - hypothetical protein YFR036w-a - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1009 |
| 3135 | 11356483 (22753, 22754) | Novel Protein sim. GBank gi 136250 sp P09380 TRNL_YEAST - TRNA LIGASE | | UNCLASSIFIED | 1058 |
| 3136 | 19883172 (12345, 12346) | Novel Protein sim. GBank gi 1363732 pir S59413 - probable membrane protein YLR454w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1001 |
| 3137 | 57292361 (17991, 17992) | Novel Protein sim. GBank gi 1363762 pir S58825 - hypothetical protein YPR195c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1024, 1027, 1034 |
| 3138 | 80308145 (13195, 13196) | Novel Protein sim. GBank gi 136482 sp P16649 TUP1_YEAST - GLUCOSE REPRESSION REGULATORY PROTEIN TUP1 (FLOCCULATION SUPPRESSOR PROTEIN (REPRESSOR AER2)) | | UNCLASSIFIED | 1006, 1025, 1029, 1039 |

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| 3139 | 20480452 (7353, 7354) | Novel Protein sim. GBank g 136593 sp P04693 TYRB_ECOLI - AROMATIC-AMINO-ACID AMINOTRANSFERASE | | UNCLASSIFIED | 1034 |
| 3140 | 78492156 (12059, 12060) | Novel Protein sim. GBank g 136936 sp P1684 JUL61_HCMVA - HYPOTHETICAL PROTEIN_U61 | | UNCLASSIFIED | 1030 |
| 3141 | 80499918 (6251, 6252) | Novel Protein sim. GBank g 1370209 emb CAA66893 - (X98238) putative; orf1 [Lactobacillus sakei] | | UNCLASSIFIED | 1012 |
| 3142 | 24144522 (1983, 1984) | Novel Protein sim. GBank g 1398238 putative; orf1 [Lactobacillus sakei] | | UNCLASSIFIED | 1053 |
| 3143 | 21432563 (2037, 2038) | Novel Protein sim. GBank g 399966 U62317 - Chromosome 22q13 BAC Clone CTT987SK-384D8 complete sequence [Homo sapiens] | | UNCLASSIFIED | 1004, 1010 |
| 3144 | 39524559 (12919, 12920) | Novel Protein sim. GBank g 140053 sp P03764 Y401_LAMBD - HYPOTHETICAL PROTEIN_ORF401 | | UNCLASSIFIED | 1006 |
| 3145 | 78463749 (4367, 4368) | Novel Protein sim. GBank g 140359 emb CAA98355 - (Z74024) hypothetical protein Rv2879c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1026 |
| 3146 | 11390288 (6097, 6098) | Novel Protein sim. GBank g 140370 sp P25567 SRO9_YEAST - SRO9 - PROTEIN | | UNCLASSIFIED | 1024 |
| 3147 | 80237180 (19633, 19634) | Novel Protein sim. GBank g 140381 sp P25744 YCEE_ECOLI - HYPOTHETICAL 43.9 KD PROTEIN IN MSYB-HTRB INTERGENIC REGION (ORF1) | | UNCLASSIFIED | 1012, 1022 |
| 3148 | 78726651 (17595, 17596) | Novel Protein sim. GBank g 140395 sp P25562 YCF4_YEAST - HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1022 |

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| 3149 22052) | 79836168 (22051, Novel Protein sim. GBank gi 140432 sp P21362 YCIF_ECOLI - 18.6 KD PROTEIN IN TONB-TRPA INTERGENIC REGION (ORF2) | | UNCLASSIFIED | 1008, 1017, 1024 |
| 3150 5914) | 78769689 (5913, Novel Protein sim. GBank gi 140514 sp P25355 YCU4_YEAST - HYPOTHETICAL 65.2 KD PROTEIN IN THR4- PWP2 INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 3151 6386) | 27931399 (6385, Novel Protein sim. GBank gi 140519 sp P25637 YCU9_YEAST - HYPOTHETICAL 29.0 KD PROTEIN IN PWP2- SUP61 INTERGENIC REGION | | UNCLASSIFIED | 1006 |
| 3152 14366) | 78785575 (14365, Novel Protein sim. GBank gi 140524 sp P25365 SED4_YEAST - SED4 PROTEIN | | UNCLASSIFIED | 1009, 1022 |
| 3153 4362) | 78983343 (4361, Novel Protein sim. GBank gi 140545 sp P25651 YCX6_YEAST - HYPOTHETICAL 21.7 KD PROTEIN IN TUP1- ABP1 INTERGENIC REGION | | UNCLASSIFIED | 1044 |
| 3154 13204) | 11122448 (13203, Novel Protein sim. GBank gi 140753 sp P26646 YHDH_ECOLI - HYPOTHETICAL 34.7 KD PROTEIN IN MREB- ACCB INTERGENIC REGION (ORF1) | | UNCLASSIFIED | 1034 |
| 3155 16040) | 79113980 (16039, Novel Protein sim. GBank gi 141279 sp P21260 YPRO_OWEFU - HYPOTHETICAL PROLINE-RICH PROTEIN | | UNCLASSIFIED | 1044 |
| 3156 14842) | 9366940 (14841, Novel Protein sim. GBank gi 141307 sp P24563 YPT4_PSEAE - HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4) | | UNCLASSIFIED | 1017 |
| 3157 19330) | 28806912 (19329, Novel Protein sim. GBank gi 141468 sp P26944 YTR6_AZOBR - HYPOTHETICAL PROTEIN IN ACETYL TRANSFERASE 3'REGION (ORF6) | | UNCLASSIFIED | 1022 |

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| 3158 | 79457254 (10729, 10730) | Novel Protein sim. GBank PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) | | UNCLASSIFIED | 1024 |
| 3159 | 55763493 (3339, 3340) | Novel Protein sim. GBank g 141617 spl P08031 ZEB2_MAIZE - ZEIN-BETA sapiens] | | UNCLASSIFIED | 1023 |
| 3160 | 88095842 (9755, 9756) | Novel Protein sim. GBank g 145484 (M93570) - PTS enzyme III cel [Escherichia coli] | | UNCLASSIFIED | 1034 |
| 3161 | 20110065 (2533, | Novel Protein sim. GBank g 146168 (J01617) - 2534) | | UNCLASSIFIED | 1010 |
| 3162 | 32081101 (11209, 11210) | Novel Protein sim. GBank g 146168 (J01617) - glutaminyl-tRNA synthetase [Escherichia coli] | | UNCLASSIFIED | 1034, 1044 |
| 3163 | 78758201 (7131, 7132) | Novel Protein sim. GBank g 14669199 dbj BAA094871 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens] | | UNCLASSIFIED | 1008 |
| 3164 | 78758215 (10153, 10154) | Novel Protein sim. GBank g 14669199 dbj BAA094871 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens] | | UNCLASSIFIED | 1008 |
| 3165 | 36998849 (12181, 12182) | Novel Protein sim. GBank g 1523984 emb CAA61455.1 - (X89084) phosphate acetyltransferase [Corynebacterium glutamicum] | | UNCLASSIFIED | 1001 |
| 3166 | 78381623 (3591, 3592) | Novel Protein sim. GBank g 1524191 emb CAE02007 - (Z79700) echA7 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1003 |
| 3167 | 66694781 (6697, 6698) | Novel Protein sim. GBank g 1524205 emb CAE01993 - (Z79700) purH [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1009 |
| 3168 | 79604009 (8439, 8440) | Novel Protein sim. GBank g 1524282 emb CAE02072 - (Z79702) uspc [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1004 |

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| 3169 | 80218307 (14651, 14652) | Novel Protein sim. GBank gi 1526613 emb CAA63821 - {X93999} alpha2,6- sialyltransferase [Mus musculus] | | UNCLASSIFIED | 1004, 1006, 1010, 1017, 1022, 1024, 1034, 1039, 1044 |
| 3170 | 13521450 (11895, 11896) | Novel Protein sim. GBank gi 1526981 emb CAA68204 - {X99945} amino acid permease YeeF like protein [Salmonella typhimurium] | | UNCLASSIFIED | 1024 |
| 3171 | 20292840 (15159, 15160) | Novel Protein sim. GBank gi 1545657 (U50396) - WbpH [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1034 |
| 3172 | 94630787 (12099, 12100) | Novel Protein sim. GBank gi 1545994 (U58366) - ArSH [Yersinia enterocolitica] | | UNCLASSIFIED | 1039 |
| 3173 | 20459785 (20431, 20432) | Novel Protein sim. GBank gi 1549276 (U68703) - hypothetical protein YdhE [Escherichia coli] | | UNCLASSIFIED | 1010 |
| 3174 | 85548752 (7029, 7030) | Novel Protein sim. GBank gi 157515 (U64899) - thrombospondin-related anonymous protein [Plasmiodium gallinaceum] | | UNCLASSIFIED | 1053 |
| 3175 | 20617093 (16857, 16858) | Novel Protein sim. GBank gi 1588980 pf 2209416K - ORF 10 [Vibrio cholerae] | | UNCLASSIFIED | 1004 |
| 3176 | 65669762 (10553, 10554) | Novel Protein sim. GBank gi 159159 (M76492) - beta-tubulin [Haemonchus contortus] | | UNCLASSIFIED | 1010 |
| 3177 | 94141819 (667, 668) | Novel Protein sim. GBank gi 1619829 (U70932) - reverse transcriptase [Peromyscus leucopus] | | UNCLASSIFIED | 1044 |
| 3178 | 79239383 (3325, 3326) | Novel Protein sim. GBank gi 1619836 (U70935) - reverse transcriptase [Peromyscus maniculatus] | | UNCLASSIFIED | 1038 |
| 3179 | 23331018 (21445, 21446) | Novel Protein sim. GBank gi 1621603 (U58365) - Np20 [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1044 |
| 3180 | 85809779 (3045, 3046) | Novel Protein sim. GBank gi 1648831 emb CA03670 - {Z81331} infB [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1048 |
| 3181 | 80248646 (20943, 20944) | Novel Protein sim. GBank gi 1651863 dbj BAA16591 - {D90899} iron(III) dicarlate transport system permease protein FecD [Synchocystis sp.] | | UNCLASSIFIED | 1006, 1009, 1024, 1034 |

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| 3182 | 27341911 (3271, 3272) | Novel Protein sim. G-Bank gi 1651871 dbj BAA16599 - (D90899) ferrichrome-iron receptor [Synechocystis sp.] | | UNCLASSIFIED | 1044 |
| 3183 | 80240187 (22173, 22174) | Novel Protein sim. G-Bank gi 1651866 dbj BAA16793 - (D90900) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1010, 1024 |
| 3184 | 9896969 (19769, 19770) | Novel Protein sim. G-Bank gi 1651867 dbj BAA16794 - (D90900) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1039 |
| 3185 | 11305577 (22089, 22090) | Novel Protein sim. G-Bank gi 1651932 dbj BAA16858 - (D90901) nitrogen fixation positive activator protein [Synechocystis sp.] | | UNCLASSIFIED | 1022 |
| 3186 | 80053608 (17799, 17800) | Novel Protein sim. G-Bank gi 1652128 dbj BAA17052 - (D90903) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1004 |
| 3187 | 7509118 (19811, 19812) | Novel Protein sim. G-Bank gi 1652190 dbj BAA17114 - (D90903) Fat protein [Synechocystis sp.] | | UNCLASSIFIED | 1058 |
| 3188 | 78380222 (5887, 5888) | Novel Protein sim. G-Bank gi 1652433 dbj BAA17355 - (D90905) SrrA [Synechocystis sp.] | | UNCLASSIFIED | 1024, 1026 |
| 3189 | 11691417 (1039, 1040) | Novel Protein sim. G-Bank gi 1652430 dbj BAA17412 - (D90905) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1034 |
| 3190 | 80508512 (22143, 22144) | Novel Protein sim. G-Bank gi 1652848 dbj BAA17766 - (D90909) DNA photolyase [Synechocystis sp.] | | UNCLASSIFIED | 1012 |
| 3191 | 79441565 (339, 340) | Novel Protein sim. G-Bank gi 1652973 dbj BAA17890 - (D90910) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1024 |
| 3192 | 88094361 (7801, 7802) | Novel Protein sim. G-Bank gi 1653184 dbj BAA18100 - (D90911) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1006, 1010, 1022, 1024, 1044 |
| 3193 | 54856619 (6593, 6594) | Novel Protein sim. G-Bank gi 1653557 dbj BAA18470 - (D90914) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1019, 1026 |

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| 3194 | 87458119 (18059) 18060) | Novel Protein sim. G-Bank gi 1655665 emb CAB03731 - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1018, 1050 |
| 3195 | 80421789 (18535, 18536) | Novel Protein sim. G-Bank gi 1655830 (U59446) - myrosinase-binding protein related protein [Brassica napus] | | UNCLASSIFIED | 1022, 1025, 1044 |
| 3196 | 13522813 (15941, 15942) | Novel Protein sim. G-Bank gi 1666113 emb CAB05059 - (Z82098) hypothetical protein Rv3547 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1024 |
| 3197 | 86472669 (1291, 1292) | Novel Protein sim. G-Bank gi 1666146 emb CAB03781 - (Z81451) hypothetical protein Rv2438c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1013, 1029 |
| 3198 | 14996187 (16231, 16232) | Novel Protein sim. G-Bank gi 1666181 emb CAB04762 - (Z82004) ORF9(1) [Rhodococcus erythropolis] | | UNCLASSIFIED | 1024 |
| 3199 | 19631884 (5537, 5538) | Novel Protein sim. G-Bank gi 1666182 emb CAB04763 - (Z82004) ORF10(1) [Rhodococcus erythropolis] | | UNCLASSIFIED | 1004 |
| 3200 | 27977959 (14813, 14814) | Novel Protein sim. G-Bank gi 1673324 dbj BAA10536 - (D64003) hypothetical protein [Synnechocystis sp.] | | UNCLASSIFIED | 1006 |
| 3201 | 80022773 (4561, 4562) | Novel Protein sim. G-Bank gi 1675226 (U67205) - ACF7 neural isoform 3 [Mus musculus] | | UNCLASSIFIED | 1034 |
| 3202 | 79630737 (21587, 21588) | Novel Protein sim. G-Bank gi 1634835 (U77671) - putative ferric siderophore receptor [Bordetella bronchiseptica] | | UNCLASSIFIED | 1023 |
| 3203 | 77918414 (20051, 20052) | Novel Protein sim. G-Bank gi 1658442 (U41417) - beta-N-acetylhexosaminidase [Vibrio furnissii] | | UNCLASSIFIED | 1036 |
| 3204 | 78911651 (10895, 10896) | Novel Protein sim. G-Bank gi 1703082 sp P53885 ACLY_CAEEL - PROBABLE ATP-CITRATE (PRO-S)-LYASE (CITRATE CLEAVAGE ENZYME) | | UNCLASSIFIED | 1017, 1022 |

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| 3205 | 19882359 (135, 136) | Novel Protein sim. GBank gi 1703229 sp P25409 ALAT_RAT - ALANINE AMINOTRANSFERASE (GLUTAMIC-PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC-ALANINE TRANSAMINASE) | UNCLASSIFIED | 1001 |
| 3206 | 71328014 (10829, 10830) | Novel Protein sim. GBank gi 1703256 sp P54918 ALR_SYN3 - ALANINE RACEMASE | UNCLASSIFIED | 1026, 1029 |
| 3207 | 78676317 (2093, 2094) | Novel Protein sim. GBank gi 1703287 sp Q11010 AMPN_STR1 - AMINOPEPTIDASE N (LYSYL AMINOPEPTIDASE) (LYS-AP) (ALANINE AMINOPEPTIDASE) | UNCLASSIFIED | 1008 |
| 3208 | 36624098 (19023, 19024) | Novel Protein sim. GBank gi 703594 (U80439) - coded for by C. elegans cDNA yk7c8.5; coded for by C. elegans cDNA yk1433b3.5; coded for by C. elegans cDNA yk65aa4.5; coded for by C. elegans cDNA yk7c8.3; coded for by C. elegans cDNA CEESQ66F; coded for by C. elegans cDNA yk65aa4.3.... | UNCLASSIFIED | 1034 |
| 3209 | 5637974 (16507, 16508) | Novel Protein sim. GBank gi 1705586 sp P52481 CAP2_RAT - ADENYL CYCLASE-ASSOCIATED PROTEIN 2 (CAP) | UNCLASSIFIED | 1058 |
| 3210 | 82125417 (227, 228) | Novel Protein sim. GBank gi 1705670 sp P40986 CC1_YEAST - CELL DIVISION CONTROL PROTEIN 1 | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1010, 1016, 1017, 1022, 1024, 1044 |
| 3211 | 78378932 (18021, 18022) | Novel Protein sim. GBank gi 1706872 sp P53603 FTCD_PIG - FORMIMINOTRANSFERASE-CYCLODEAMINASE (FTCD) (GLUTAMATE FORMIMINOTRANSFERASE (GLUTAMATE FORMYLTRANSFERASE) / FORMIMINOTETRAHYDROFOLATE CYCLODEAMINASE) | UNCLASSIFIED | 1003 |

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| 3212 | 95009485 (10877, 10878) | Novel Protein sim. GBank gi 1707846 emb CAA67865 - (X99514) opin [Pseudomonas aeruginosa] | | | |
| 3213 | 79626814 (16673, 16674) | Novel Protein sim. GBank gi 1708007 sp P50457 GOAG_ECOLI - 4-AMINOBUTYRATE AMINOTRANSFERASE (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA TRANSAMINASE) (GLUTAMATE:SUCINIC SEMIALDEHYDE TRANSAMINASE) (GABA AMINOTRANSFERASE) | | UNCLASSIFIED | 1004 |
| 3214 | 65848327 (4933, 4934) | Novel Protein sim. GBank gi 1708021 sp P51653 GPC2_RAT - GLYCAN-2 PRECURSOR (CEREBROGLYCAN) (HSPG M13) | | UNCLASSIFIED | 1025, 1054 |
| 3215 | 20378295 (5639, 5640) | Novel Protein sim. GBank gi 1708180 sp Q10602 HEMK_MYCTU - HEMK PROTEIN HOMOLOG | | UNCLASSIFIED | 1004 |
| 3216 | 79470088 (3985, 3986) | Novel Protein sim. GBank gi 1708195 sp P51979 HFM1_YEAST - HFM1 PROTEIN | | UNCLASSIFIED | 1022 |
| 3217 | 79565161 (20551, 20552) | Novel Protein sim. GBank gi 1709029 sp P53258 MIC1_YEAST - MIC1 PROTEIN | | UNCLASSIFIED | 1023 |
| 3218 | 7432119 (7989, 7990) | Novel Protein sim. GBank gi 1709062 sp P50108 MNN10_YEAST - GALACTOSYLTRANSFERASE MNN10 (BUD EMERGENCE DELAY PROTEIN 1) | | UNCLASSIFIED | 1058 |
| 3219 | 78498831 (18573, 18574) | Novel Protein sim. GBank gi 1709250 sp P46935 NED4_MOUSE - NEDD-4 PROTEIN | | UNCLASSIFIED | 1008, 1026 |
| 3220 | 87123187 (5819, 5820) | Novel Protein sim. GBank gi 1710106 sp Q10606 RFE_MYCTU - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE | | UNCLASSIFIED | 1007, 1012, 1022, 1023, 1026, 1029, 1030, 1034 |

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| 3221 | 80229862 (1267, 1268) | Novel Protein sim. GBank g 1710241 (U79274) - unknown [Homo sapiens] | | UNCLASSIFIED | 1022, 1024, 1034, 1038 |
| 3222 | 11286147 (22271, 22272) | Novel Protein sim. GBank g 171057 (M29146) - alpha-mannosidase [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1006, 1058 |
| 3223 | 8488632 (3269, 3270) | Novel Protein sim. GBank g 1710594 sp P5352 RLR1_YEAST - RLR1 PROTEIN | | UNCLASSIFIED | 1022 |
| 3224 | 82335498 (11549, 11550) | Novel Protein sim. GBank g 1710803 sp P32608 RTG2_YEAST - RETROGRADE REGULATION PROTEIN 2 | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1016, 1017, 1022, 1024, 1029, 1034, 1044 |
| 3225 | 21629450 (3033, 3034) | Novel Protein sim. GBank g 1711345 sp P53012 SCS3_YEAST - SCS3 PROTEIN | | UNCLASSIFIED | 1008, 1034 |
| 3226 | 11611950 (771, 772) | Novel Protein sim. GBank g 1711360 sp P55021 SECA_STRLI - PREPROTEIN TRANSLOCASE SECA SUBUNIT | | UNCLASSIFIED | 1006 |
| 3227 | 13517742 (6451, 6452) | Novel Protein sim. GBank g 1711360 sp P55021 SECA_STRLI - PREPROTEIN TRANSLOCASE SECA SUBUNIT | | UNCLASSIFIED | 1024 |
| 3228 | 52563118 (21539, 21540) | Novel Protein sim. GBank g 1711364 sp P15599 STS_RAT - STERYL-SULFATASE PRECURSOR (STEROID SULFATASE) (STEREYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) | | UNCLASSIFIED | 1006, 1026 |
| 3229 | 30005352 (8115, 8116) | Novel Protein sim. GBank g 171485 (L07289) - ESP1 gene product [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1009 |

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| 3230 | 79448778 (15853) | Novel Protein sim. GBank gil171615 (J0369) - nucleotide-binding regulatory protein GPA2 [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1008, 1034 |
| 3231 | 56145263 (2451, 2452) | Novel Protein sim. GBank gil1718245 (U69488) - viral envelope like protein [Mus musculus] | | UNCLASSIFIED | 1008 |
| 3232 | 80054070 (235, 236) | Novel Protein sim. GBank gil171940 (M84455) - leucine zipper protein [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1017, 1022 |
| 3233 | 82112527 (7383, 7384) | Novel Protein sim. GBank gil171940 (M84455) - leucine zipper protein [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1003, 1006, 1008, 1016, 1017, 1022, 1024, 1027, 1034, 1038, 1039 |
| 3234 | 80062380 (2887, 2888) | Novel Protein sim. GBank gil172094 (M36822) - SIN3 open reading frame [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1003, 1004, 1010 |
| 3235 | 80500184 (6607, 6608) | Novel Protein sim. GBank gil1722927 sp Q10403 Y00R_MYCTU - HYPOTHETICAL 31.7 KD PROTEIN CY190.27 | | UNCLASSIFIED | 1003, 1004, 1006, 1010, 1012, 1017, 1024, 1030, 1034, 1039 |
| 3236 | 78676067 (6017, 6018) | Novel Protein sim. GBank gil1722945 sp Q10523 Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427.23 | | UNCLASSIFIED | 1008 |
| 3237 | 82124947 (17637, 17638) | Novel Protein sim. GBank gil1722971 sp Q10638 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C | | UNCLASSIFIED | 1004, 1006, 1008, 1010, 1016, 1022, 1029 |
| 3238 | 79914416 (18307, 18308) | Novel Protein sim. GBank gil1723026 sp Q10897 Y05L_MYCTU - HYPOTHETICAL 70.4 KD PROTEIN CY251.21 | | UNCLASSIFIED | 1001 |
| 3239 | 47652140 (11739, 11740) | Novel Protein sim. GBank gil1723065 sp Q11030 Y07O_MYCTU - HYPOTHETICAL 37.3 KD PROTEIN CY02B10.24 PRECURSOR | | UNCLASSIFIED | 1029 |

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| 3240 | 79589353 (19353, 19354) | Novel Protein sim. GBank g 1723092 sp Q11059 Y08N_MYCTU- HYPOTHETICAL 37.0 KD PROTEIN CY50.23C | | UNCLASSIFIED | 1010, 1038 |
| 3241 | 80218509 (19505, 19506) | Novel Protein sim. GBank g 1723189 sp P39731 YADA_YEAST- HYPOTHETICAL 33.2 KD PROTEIN IN PYK1- SNC1 INTERGENIC REGION | | UNCLASSIFIED | 1010, 1017, 1022, 1024, 1025, 1031, 1034, 1044 |
| 3242 | 80250304 (1989, 1990) | Novel Protein sim. GBank g 1723558 sp Q10449 YDEG_SCHPO- HYPOTHETICAL 57.2 KD PROTEIN C12B10.16C IN CHROMOSOME I | | UNCLASSIFIED | 1006 |
| 3243 | 80229661 (19319, 19320) | Novel Protein sim. GBank g 1723543 sp P53204 YG15_YEAST- HYPOTHETICAL 44.9 KD PROTEIN IN SEC9- MSB2 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1024, 1044 |
| 3244 | 27842185 (15643, 15644) | Novel Protein sim. GBank g 1723550 sp P53212 YG1D_YEAST- HYPOTHETICAL 31.7 KD PROTEIN IN VMA7- RPSS1A INTERGENIC REGION | | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1034 |
| 3245 | 79608932 (13893, 13894) | Novel Protein sim. GBank g 1723588 sp P53255 YG2M_YEAST- HYPOTHETICAL 58.2 KD PROTEIN IN DBF2- VAS1 INTERGENIC REGION | | UNCLASSIFIED | 1034 |
| 3246 | 80478615 (7461, 7462) | Novel Protein sim. GBank g 1723591 sp P53267 YG2Y_YEAST- HYPOTHETICAL 37.8 KD PROTEIN IN CLB6- SPT6 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1010, 1012, 1017, 1022, 1024, 1025, 1027, 1034 |
| 3247 | 80219848 (18267, 18268) | Novel Protein sim. GBank g 1723699 sp P53267 YG2Y_YEAST- HYPOTHETICAL 37.8 KD PROTEIN IN CLB6- SPT6 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1010, 1022, 1024, 1034, 1039 |

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| 3248 | 9896921 (10627, 10628) | Novel Protein sim. GBank gi 1723811 sp P55135 YGCA_ECOLI - HYPOTHETICAL RNA METHYLTRANSFERASE IN RELA-BARA INTERGENIC REGION | | UNCLASSIFIED | 1039 |
| 3249 | 80016773 (18085, 18086) | Novel Protein sim. GBank gi 1723900 sp P53140 YGK7_YEAST - HYPOTHETICAL 74.6 KD PROTEIN IN TAF60- G4P1 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1006, 1010, 1012, 1022 |
| 3250 | 29235305 (6345, 6346) | Novel Protein sim. GBank gi 1723969 sp P53075 YGX8_YEAST - HYPOTHETICAL 66.9 KD PROTEIN IN SAP4- OST5 INTERGENIC REGION | | UNCLASSIFIED | 1008 |
| 3251 | 95011210 (21421, 21422) | Novel Protein sim. GBank gi 1723971 sp P53067 YGZ1_YEAST - HYPOTHETICAL 113.9 KD PROTEIN IN RTF1- CSE1 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1008, 1022, 1038 |
| 3252 | 11612706 (6357, 6358) | Novel Protein sim. GBank gi 1723981 sp P53063 YGZ6_YEAST - HYPOTHETICAL 44.5 KD PROTEIN IN PDE1- RTF1 INTERGENIC REGION | | UNCLASSIFIED | 1006 |
| 3253 | 24122000 (1697, 1698) | Novel Protein sim. GBank gi 1723978 embj CAA70932 - (Y09798) colS [Pseudomonas fluorescens] | | UNCLASSIFIED | 1044 |
| 3254 | 78300843 (8207, 8208) | Novel Protein sim. GBank gi 1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT) | | UNCLASSIFIED | 1026, 1030 |
| 3255 | 57303999 (16043, 16044) | Novel Protein sim. GBank gi 1730592 sp P49954 YI85_YEAST - HYPOTHETICAL 32.5 KD PROTEIN YLR351C | | UNCLASSIFIED | 1034 |
| 3256 | 79776164 (1177, 1178) | Novel Protein sim. GBank gi 1730621 sp P53759 YMI0_YEAST - HYPOTHETICAL 48.1 KD PROTEIN IN TUB1- CPR3 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1008 |

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| 3257 | 20705686 (7727, 7728) | Novel Protein sim. GBank gi 11730632 sp P50104 YMP9_YEAST - PUTATIVE 109.8 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN SOK2-FMS1 INTERGENIC REGION | UNCLASSIFIED | 1034 |
| 3258 | 78444803 (12925, 12926) | Novel Protein sim. GBank gi 11730647 sp P53632 YN23_YEAST - HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECURSOR | UNCLASSIFIED | 1026 |
| 3259 | 71088488 (18455, 18456) | Novel Protein sim. GBank gi 11730647 sp P53832 YN23_YEAST - HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECURSOR | UNCLASSIFIED | 1029, 1053 |
| 3260 | 80218785 (10043, 10044) | Novel Protein sim. GBank gi 11730655 sp P53824 SNZ2_YEAST - SNZ2 PROTEIN | UNCLASSIFIED | 1003, 1006, 1010, 1022, 1024, 1031, 1034 |
| 3261 | 80219860 (21489, 21490) | Novel Protein sim. GBank gi 11730730 sp P53954 ALGB_YEAST - ALG11 PROTEIN | UNCLASSIFIED | 1004, 1006, 1009, 1010, 1024 |
| 3262 | 78725687 (20185, 20186) | Novel Protein sim. GBank gi 11730733 sp P53951 YNF1_YEAST - HYPOTHETICAL 45.6 KD PROTEIN IN COX5A-ALG11 INTERGENIC REGION | UNCLASSIFIED | 1022 |
| 3263 | 79600647 (18433, 18434) | Novel Protein sim. GBank gi 11730746 sp P53939 YNH8_YEAST - HYPOTHETICAL 45.9 KD PROTEIN IN TPM1-MKS1 INTERGENIC REGION | UNCLASSIFIED | 1006 |
| 3264 | 80219252 (1085, 1086) | Novel Protein sim. GBank gi 11730751 sp P53935 YNJ1_YEAST - HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1016, 1017, 1022, 1023, 1024, 1031, 1034, 1039, 1044 |

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| 3266 | 38909150 (19221, 19222) | Novel Protein sim. GBank gil1730764 sp P53927 YNL0_YEAST - HYPOTHETICAL 25.4 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION | UNCLASSIFIED | 1008 |
| 3266 | 80236379 (3495, 3496) | Novel Protein sim. GBank gil1730773 sp P53918 YNM5_YEAST - HYPOTHETICAL 73.8 KD PROTEIN IN SPC98-TOM70 INTERGENIC REGION | UNCLASSIFIED | 1008, 1009, 1024 |
| 3267 | 27959515 (21835, 21836) | Novel Protein sim. GBank gil1730779 sp P53912 YNN4_YEAST - HYPOTHETICAL 41.2 KD PROTEIN IN FPR1-TOM22 INTERGENIC REGION | UNCLASSIFIED | 1006 |
| 3268 | 25324266 (7897, 7898) | Novel Protein sim. GBank gil1730799 sp P53890 YNQ6_YEAST - HYPOTHETICAL 49.7 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION | UNCLASSIFIED | 1017 |
| 3269 | 20182193 (17951, 17952) | Novel Protein sim. GBank gil1730815 sp P53873 YNS7_YEAST - HYPOTHETICAL 40.3 KD PROTEIN IN KAR1-UBP10 INTERGENIC REGION | UNCLASSIFIED | 1024 |
| 3270 | 79556251 (19679, 19680) | Novel Protein sim. GBank gil1730823 sp P53888 ALG9_YEAST - PROBABLE MANNOSEYLTRANSFERASE ALG9 | UNCLASSIFIED | 1025 |
| 3271 | 56011990 (11911, 11912) | Novel Protein sim. GBank gil1731071 sp P54545 YQJH_BACSU - HYPOTHETICAL 47.0 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION | UNCLASSIFIED | 1008 |
| 3272 | 78082991 (975, 976) | Novel Protein sim. GBank gil1731094 sp P54571 YQKL_BACSU - HYPOTHETICAL NA+/H+ ANTIPORTER IN ANSB-SPOIIM INTERGENIC REGION | UNCLASSIFIED | 1029 |
| 3273 | 20731645 (6543, 6544) | Novel Protein sim. GBank gil1731125 sp P54433 YRKF_BACSU - HYPOTHETICAL 20.7 KD PROTEIN IN BLTR-SPOIIIIC INTERGENIC REGION | UNCLASSIFIED | 1034 |

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| 3274 | 80258978 (16471, 16472) | Novel Protein sim. GBank gil1731287 splQ10818 YX28_MYCTU - HYPOTHETICAL 52.9 KD PROTEIN CY274.28C | UNCLASSIFIED | 1022, 1026, 1030 |
| 3275 | 20724406 (11513, 11514) | Novel Protein sim. GBank gil1731295 splQ10827 YX42_MYCTU - HYPOTHETICAL 17.0 KD PROTEIN CY274.42C | UNCLASSIFIED | 1006 |
| 3276 | 54656911 (17058, 17060) | Novel Protein sim. GBank gil1731438 splIP51504 ZN80_HUMAN - ZINC FINGER PROTEIN 80 [ZNFPPT17] | UNCLASSIFIED | 1022 |
| 3277 | 5628381 (13397, 13398) | Novel Protein sim. GBank gil173164 (J02719) - valyl-tRNA synthetase [Saccharomyces cerevisiae] | UNCLASSIFIED | 1058 |
| 3278 | 79625428 (507, 508) | Novel Protein sim. GBank gil173177 (L02869) - VPS17 [Saccharomyces cerevisiae] | UNCLASSIFIED | 1006, 1022, 1023, 1026, 1044 |
| 3279 | 80232516 (18025, 18026) | Novel Protein sim. GBank gil1736514 dbj BAA15678 - (D90829) Isochorismatase [EC 3.3.2.1] (2,3 dihydro-2,3 dihydroxybenzoate synthase). [Escherichia coli] | UNCLASSIFIED | 1022 |
| 3280 | 82021119 (10167, 10168) | Novel Protein sim. GBank gil1742619 dbj BAA15320 - (D90801) Bicyclomycin resistance protein (Sulfonamide resistance protein). [Escherichia coli] | UNCLASSIFIED | 1003, 1006, 1010, 1016, 1022, 1023, 1026, 1029, 1039, 1049, 1054 |
| 3281 | 52560843 (16125, 16126) | Novel Protein sim. GBank gil1742728 dbj BAA15421 - (D90809) Chitinase 3 precursor [EC 3.2.1.14]. [Escherichia coli] | UNCLASSIFIED | 107 |
| 3282 | 80428437 (7339, 7340) | Novel Protein sim. GBank gil1742766 dbj BAA15457 - (D90811) NifS protein. [Escherichia coli] | UNCLASSIFIED | 1023, 1025, 1054 |
| 3283 | 27980533 (14451, 14452) | Novel Protein sim. GBank gil1750108 (U66480) - YnbA [Bacillus subtilis] | UNCLASSIFIED | 1006 |
| 3284 | 79551776 (21291, 21292) | Novel Protein sim. GBank gil1753160 (U79564) - unidentified ferric siderophore receptor [Bordetella bronchiseptica] | UNCLASSIFIED | 1001 |

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| 3285 | 55310325 (12997, 12998) | Novel Protein sim. GBank gil1754627[db]BAA13116 - (D86566) NOTCH4 [Homo sapiens] | | UNCLASSIFIED | 1019 |
| 3286 | 17650051 (21473, 21474) | Novel Protein sim. GBank gil1763011 (U67963) - lysophospholipase homolog [Homo sapiens] | | UNCLASSIFIED | 1017 |
| 3287 | 79179312 (2357, 2358) | Novel Protein sim. GBank gil1780764[emb]CAB71456 - (Y10435) translated orf similarity to SWISS-PROT: SYGA_ECOLI glycyl-tRNA synthetase alpha-chain [Coxiella burnetii] | | UNCLASSIFIED | 1024 |
| 3288 | 20742752 (18699, 18700) | Novel Protein sim. GBank gil1781050[emb]CAB06186 - (Z83863) aroE [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1022 |
| 3289 | 79764293 (7335, 7336) | Novel Protein sim. GBank gil1781122[emb]CAB06206 - (Z83864) hypothetical protein Rv3835 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1023, 1034, 1044 |
| 3290 | 95293316 (16855, 16856) | Novel Protein sim. GBank gil1781144[emb]CAB06254 - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1024 |
| 3291 | 20402955 (22433, 22434) | Novel Protein sim. GBank gil1781185[emb]CAB06125 - (Z83859) adhA [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1004 |
| 3292 | 65707949 (5475, 5476) | Novel Protein sim. GBank gil1787094 (AE000188) - putative dTDP-glucose enzyme [Escherichia coli] | | UNCLASSIFIED | 1023, 1031 |
| 3293 | 93228207 (6809, 6810) | Novel Protein sim. GBank gil1787243 (AE000202) - putative enzyme [Escherichia coli] | | UNCLASSIFIED | 1003 |
| 3294 | 13022355 (10073, 10074) | Novel Protein sim. GBank gil1787247 (AE000202) - orf, hypothetical protein [Escherichia coli] | | UNCLASSIFIED | 1024 |
| 3295 | 79863168 (3073, 3074) | Novel Protein sim. GBank gil1787723 (AE000242) - putative outer membrane receptor for iron transport [Escherichia coli] | | UNCLASSIFIED | 1017 |

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| 3296 | 17710632 (6727, 6728) | Novel Protein sim. GBank gil1787723 (AE000242) - putative outer membrane receptor for iron transport [Escherichia coli] | UNCLASSIFIED | 1044 |
| 3297 | 10056612 (7459, 7460) | Novel Protein sim. GBank gil1787724 (AE000242) - putative receptor [Escherichia coli] | UNCLASSIFIED | 1017 |
| 3298 | 8355488 (21367, 21368) | Novel Protein sim. GBank gil1788590 (AE000315) - orf, hypothetical protein [Escherichia coli] | UNCLASSIFIED | 1008, 1022 |
| 3299 | 78677629 (17171, 17172) | Novel Protein sim. GBank gil1788627 (AE000318) - putative aminotransferase [Escherichia coli] | UNCLASSIFIED | 1009 |
| 3300 | 20398139 (3733, 3734) | Novel Protein sim. GBank gil1788770 (AE000330) - putative beta-lactamase [Escherichia coli] | UNCLASSIFIED | 1004 |
| 3301 | 79629423 (17999, 18000) | Novel Protein sim. GBank gil1789035 (AE000352) - orf, hypothetical protein [Escherichia coli] | UNCLASSIFIED | 1003 |
| 3302 | 13515530 (14619, 14620) | Novel Protein sim. GBank gil1789036 (AE000352) - putative transport protein [Escherichia coli] | UNCLASSIFIED | 1024 |
| 3303 | 20445442 (15505, 15506) | Novel Protein sim. GBank gil1790277 (AE000459) - putative oxidoreductase [Escherichia coli] | UNCLASSIFIED | 1010 |
| 3304 | 70945165 (21979, 21920) | Novel Protein sim. GBank gil1794165 dbj BAA112 5 - (D78137) Na+/glucose symporter [Vibrio parahaemolyticus] | UNCLASSIFIED | 1029 |
| 3305 | 77539953 (6019, 6020) | Novel Protein sim. GBank gil1800301 (U83667) - macrolide-efflux determinant [Streptococcus pneumoniae] | UNCLASSIFIED | 1016 |
| 3306 | 20451216 (15991, 15992) | Novel Protein sim. GBank gil1817699 emb CAB06573I - (Z84724) hypothetical protein Rv0433 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1024 |

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|------|----------------------------|---|--|--------------|---------------------------|
| 3307 | 25252782 (5691, 5692) | Novel Protein sim. GBank gii1817714 emb CAB06590 - (Z84725) pqK [Mycobacterium tuberculosis] | | UNCLASSIFIED | |
| 3308 | 32302946 (10315, 10316) | Novel Protein sim. GBank gii1834378 emb CAA70860 - (Y09666) RagB [Bradyrhizobium japonicum] | | UNCLASSIFIED | 1029 |
| 3309 | 80504793 (22535, 22536) | Novel Protein sim. GBank gii1838990 emb CAB06634 - (Z85982) hypothetical protein Rv1639c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012 |
| 3310 | 20465379 (9341, 9342) | Novel Protein sim. GBank gii1838991 emb CAB06635 - (Z85982) lysX [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1010 |
| 3311 | 66490267 (15309, 15310) | Novel Protein sim. GBank gii1842429 (U81036) - ankyrin binding cell adhesion molecule neurofascin [Rattus norvegicus] | | UNCLASSIFIED | 1010, 1029 |
| 3312 | 79561132 (1237, 1238) | Novel Protein sim. GBank gii1848058 dbj BAA11346 - (D78321) pyrimidine dimer DNA glycosylase [Microccocus luteus] | | UNCLASSIFIED | 1038 |
| 3313 | 37034313 (19689, 19690) | Novel Protein sim. GBank gii1850114 emb CAB06681 - (Z86089) hypothetical protein Rv0269c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012 |
| 3314 | 86688786 (12397, 12398) | Novel Protein sim. GBank gii186396 (M94131) - mucin [Homo sapiens] | | UNCLASSIFIED | 1018, 1024, 1029, 1038 |
| 3315 | 54534348 (7103, 7104) | Novel Protein sim. GBank gii186398 (M94132) - MUC2 [Homo sapiens] | | UNCLASSIFIED | 1041 |
| 3316 | 27977681 (321, 322) | Novel Protein sim. GBank gii1870004 emb CAB06855 - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1006 |
| 3317 | 19536322 (5025, 5026) | Novel Protein sim. GBank gii1870004 emb CAB06855 - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1039 |

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| 3318 | 79862802 (13485, 13486) | Novel Protein sim. GBank gil1877288[emb CAB07049] - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1010, 1012, 1049 |
| 3319 | 14988129 (10937, 10938) | Novel Protein sim. GBank gil1877371[emb CAB07123] - (Z92772) hypothetical protein Rv0634c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1001 |
| 3320 | 80075653 (12217, 12218) | Novel Protein sim. GBank gil188864 (M74027) - mucin [Homo sapiens] | | UNCLASSIFIED | 1017, 1034 |
| 3321 | 9674619 (22667, 22668) | Novel Protein sim. GBank gil1905993 (UB9712) - putative 3-(3-hydroxyphenyl) propionate transport protein; HppK [Rhodococcus globerulus] | | UNCLASSIFIED | 1034 |
| 3322 | 20586591 (1551, 1552) | Novel Protein sim. GBank gil1934732 (U96128) - UDP-galactopyranose mutase [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1022 |
| 3323 | 20544489 (11809, 11810) | Novel Protein sim. GBank gil1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans] | | UNCLASSIFIED | 1058 |
| 3324 | 78726670 (19809, 19810) | Novel Protein sim. GBank gil1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans] | | UNCLASSIFIED | 1008, 1054 |
| 3325 | 90999628 (7327, 7328) | Novel Protein sim. GBank gil198646 (M29324) - ORF2; 5' end undetermined. [Mus musculus] | | UNCLASSIFIED | 1020 |
| 3326 | 20467349 (763, 764) | Novel Protein sim. GBank gil2039375 (U97405) - T09B4.5 gene product [Caenorhabditis elegans] | | UNCLASSIFIED | 1010 |
| 3327 | 65484068 (10063, 10064) | Novel Protein sim. GBank gil2047346 (AF000198) - Similar to cuticular collagen [Caenorhabditis elegans] | | UNCLASSIFIED | 1001, 1023 |
| 3328 | 80236408 (16339, 16340) | Novel Protein sim. GBank gil2055394 (UB7306) - transmembrane receptor UNC5H2 [Rattus norvegicus] | | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1023, 1024, 1034 |

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| 3329 | 65866027 (16111, 16112) | Novel Protein sim. GBank gi 2065209 emb CAA73250 - ('Y12713) Gag polyprotein [Mus musculus] | | UNCLASSIFIED | 1038 |
| 3330 | 78391858 (16961, 16962) | Novel Protein sim. GBank gi 2065210 emb CAA73251 - ('Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus] | | UNCLASSIFIED | 1030 |
| 3331 | 79474456 (17017, 17018) | Novel Protein sim. GBank gi 2065210 emb CAA73251 - ('Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus] | | UNCLASSIFIED | 1038 |
| 3332 | 20746461 (21773, 21774) | Novel Protein sim. GBank gi 2065210 emb CAA73251 - ('Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus] | | UNCLASSIFIED | 1004 |
| 3333 | 868666767 (21889, 21890) | Novel Protein sim. GBank gi 2072719 emb CAB08323 - (Z95121) hypothetical protein Rv3252c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1029 |
| 3334 | 86684161 (9373, 9374) | Novel Protein sim. GBank gi 2072966 (U93570) - p40 [Homo sapiens] | | UNCLASSIFIED | 1029 |
| 3335 | 65881389 (21373, 21374) | Novel Protein sim. GBank gi 2072967 (U93570) - putative p150 [Homo sapiens] | | UNCLASSIFIED | 1054 |
| 3336 | 78376411 (2139, 2140) | Novel Protein sim. GBank gi 2076703 emb CAB08362 - (Z95150) hypothetical protein Rv3129 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1008, 1026 |
| 3337 | 88097287 (6161, 6162) | Novel Protein sim. GBank gi 2078009 emb CAB08456 - (Z95207) hypothetical protein Rv2850c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1008, 1013, 1018, 1019, 1025, 1026, 1029, 1053, 1054 |
| 3338 | 80052457 (1105, 1106) | Novel Protein sim. GBank gi 2078027 emb CAB08467 - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1010, 1017 |
| 3339 | 82103445 (16203, 16204) | Novel Protein sim. GBank gi 2078037 emb CAB08461 - (Z95208) hypothetical protein Rv2362c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1003, 1004, 1016, 1017, 1022, 1024 |

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|------|-------------------------|--|--------------|------------|
| 3340 | 77887412 (8899, 8900) | Novel Protein sim. GBank gi 2078043 emb CAB084661 - (Z95208) glyS [Mycobacterium tuberculosis] Novel Protein sim. GBank gi 2088651 (AF002109) - hypersensitivity-related gene 201 (isolog [Arabidopsis thaliana]) | UNCLASSIFIED | 1023 |
| 3341 | 79167914 (19061, 19062) | Novel Protein sim. GBank gi 2088651 (AF002109) - hypersensitivity-related gene 201 (isolog [Arabidopsis thaliana]) | UNCLASSIFIED | 1031, 1050 |
| 3342 | 80504299 (14935, 14936) | Novel Protein sim. GBank gi 208931 (M15619) - ORF 6-lacZ fusion protein [Artificial gene] | UNCLASSIFIED | 1012 |
| 3343 | 17679564 (20209, 20210) | Novel Protein sim. GBank gi 2104302 emb CAB086311 - (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1008 |
| 3344 | 78386187 (21501, 21502) | Novel Protein sim. GBank gi 2104315 emb CAB086641 - (Z95388) ppbB [Mycobacterium tuberculosis] | UNCLASSIFIED | 1008 |
| 3345 | 79911261 (20103, 20104) | Novel Protein sim. GBank gi 2104343 emb CAB086581 - (Z95388) hypothetical protein Rv2135c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1012 |
| 3346 | 88094709 (15027, 15028) | Novel Protein sim. GBank gi 2104352 emb CAB086901 - (Z95389) mrsa [Mycobacterium tuberculosis] | UNCLASSIFIED | 1004 |
| 3347 | 79872123 (18527, 18528) | Novel Protein sim. GBank gi 2104361 emb CAB087291 - (Z95390) hypothetical protein Rv3463 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1044 |
| 3348 | 78993157 (905, 906) | Novel Protein sim. GBank gi 2104465 emb CAB087751 - (Z95397) unknown [Schizosaccharomyces pombe] | UNCLASSIFIED | 1039 |
| 3349 | 20294822 (21991, 21992) | Novel Protein sim. GBank gi 2105045 emb CAB088391 - (Z95436) hypothetical protein Rv3649 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1034 |
| 3350 | 79413302 (14019, 14020) | Novel Protein sim. GBank gi 2113919 emb CAB088881 - (Z95554) hypothetical protein Rv1635c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1024 |

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| 3351 | 78475152 (16965, 16966) | Novel Protein sim. GBank gi 2113941 emb CAB08926 - (Z95556) hypothetical protein Rv2508c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1003, 1006 |
| 3352 | 78368412 (5391, 5392) | Novel Protein sim. GBank gi 2114020 emb CAB08969 - (Z95558) [Mycobacterium tuberculosis] | UNCLASSIFIED | 1003 |
| 3353 | 19520527 (1333, 1334) | Novel Protein sim. GBank gi 2114024 emb CAB08957 - (Z95558) [Mycobacterium tuberculosis] | UNCLASSIFIED | 1022 |
| 3354 | 78459337 (8593, 8594) | Novel Protein sim. GBank gi 2114321 dbj BAA20037 - (D88733) membrane glycoprotein [Equine herpesvirus 1] | UNCLASSIFIED | 1016, 1026, 1029 |
| 3355 | 80258073 (11169, 11170) | Novel Protein sim. GBank gi 2114321 dbj BAA20037 - (D88733) membrane glycoprotein [Equine herpesvirus 1] | UNCLASSIFIED | 1010 |
| 3356 | 11669239 (16597, 16598) | Novel Protein sim. GBank gi 2114321 dbj BAA20037 - (D88733) membrane glycoprotein [Equine herpesvirus 1] | UNCLASSIFIED | 1024 |
| 3357 | 99277458 (16935, 16936) | Novel Protein sim. GBank gi 2114323 dbj BAA20038 - (D88734) membrane glycoprotein [Equine herpesvirus 1] | UNCLASSIFIED | 1001, 1003, 1004, 1008, 1009, 1010, 1017, 1022, 1023, 1031, 1034, 1037, 1038, 1039, 1040, 1044, 1049, 1053, 1054 |
| 3358 | 56718862 (10925, 10926) | Novel Protein sim. GBank gi 2114473 U96663 - p140mDia [Mus musculus] | UNCLASSIFIED | 1000, 1017 |
| 3359 | 12882700 (18713, 18714) | Novel Protein sim. GBank gi 2117191 emb CAB09012 - (Z95584) [Mycobacterium tuberculosis] | UNCLASSIFIED | 1031 |
| 3360 | 27954841 (657, 658) | Novel Protein sim. GBank gi 2117310 emb CAB09116_1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe] | UNCLASSIFIED | 1022 |

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| 3361 | 80080798 (1645, 1646) | Novel Protein sim. GBank gi 2117310 emb CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1023, 1034 |
| 3362 | 20297171 (3101, 3102) | Novel Protein sim. GBank gi 2117310 emb CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1034 |
| 3363 | 80049510 (20545, 20546) | Novel Protein sim. GBank gi 2117310 emb CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1010 |
| 3364 | 79444139 (9831, 9832) | Novel Protein sim. GBank gi 2120075 pir S69966 - TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty2.L | | UNCLASSIFIED | 1003, 1008, 1010 |
| 3365 | 34623202 (4159, 4160) | Novel Protein sim. GBank gi 2120083 pir I38588 - transposon LRE2 reverse transcriptase homolog - human | | UNCLASSIFIED | 1029 |
| 3366 | 78380212 (4809, 4810) | Novel Protein sim. GBank gi 2127337 pir I40661 - methylaspartate mutase (EC 5.4.99.1) component L - Clostridium cochlearium | | UNCLASSIFIED | 1026 |
| 3367 | 78795030 (12323, 12324) | Novel Protein sim. GBank gi 2127352 pir I40866 - exo-alpha-stalidase (EC 3.2.1.18) - Clostridium perfringens | | UNCLASSIFIED | 1008, 1022, 1053 |
| 3368 | 80502586 (15215, 15216) | Novel Protein sim. GBank gi 2127352 pir I40866 - exo-alpha-stalidase (EC 3.2.1.18) - Clostridium perfringens | | UNCLASSIFIED | 1012, 1023, 1024, 1036 |
| 3369 | 79610404 (8339, 8340) | Novel Protein sim. GBank gi 2127414 pir S60084 - hypothetical protein 2 - Corynebacterium glutamicum | | UNCLASSIFIED | 1004 |
| 3370 | 39290717 (22223, 22224) | Novel Protein sim. GBank gi 2128914 pir F64489 - hypothetical protein MJ1519 - Methanococcus jannaschii | | UNCLASSIFIED | 1029 |

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| 3371 | 30656520 (10363, 10364) | Novel Protein sim. GBank gij2129003 pir G64507 hypothetical protein MJ1665 - Methanococcus jannaschii | | UNCLASSIFIED | 1026 |
| 3372 | 79399335 (16829, 16830) | Novel Protein sim. GBank gij2129003 pir G64507 hypothetical protein MJ1665 - Methanococcus jannaschii | | UNCLASSIFIED | 1024 |
| 3373 | 79582628 (16871, 16872) | Novel Protein sim. GBank gij2129003 pir G64507 hypothetical protein MJ1665 - Methanococcus jannaschii | | UNCLASSIFIED | 1027 |
| 3374 | 47656049 (3687, 3688) | Novel Protein sim. GBank gij2129478 pir S51939 chitinase (EC 3.2.1.14) precursor - beet | | UNCLASSIFIED | 1004, 1029 |
| 3375 | 37815406 (5483, 5484) | Novel Protein sim. GBank gij2129478 pir S51939 chitinase (EC 3.2.1.14) precursor - beet | | UNCLASSIFIED | 1058 |
| 3376 | 79779788 (12603, 12604) | Novel Protein sim. GBank gij2129478 pir S51939 chitinase (EC 3.2.1.14) precursor - beet | | UNCLASSIFIED | 1017 |
| 3377 | 21144927 (18887, 18888) | Novel Protein sim. GBank gij2129478 pir S51939 chitinase (EC 3.2.1.14) precursor - beet | | UNCLASSIFIED | 1034 |
| 3378 | 791175240 (3543, 3544) | Novel Protein sim. GBank gij2129582 pir S71227 extensin 1 - Arabidopsis thaliana | | UNCLASSIFIED | 1001, 1024, 1037 |
| 3379 | 20197511 (22615, 22616) | Novel Protein sim. GBank gij2129777 pir S71185 ribonucleoprotein - Arabidopsis thaliana | | UNCLASSIFIED | 1010 |
| 3380 | 79966403 (13029, 13030) | Novel Protein sim. GBank gij2129803 pir S80611 probable serine/threonine-specific protein kinase (EC 2.7.1.-) BSK2 - rape | | UNCLASSIFIED | 1003 |
| 3381 | 80026647 (11015, 11016) | Novel Protein sim. GBank gij2131050 emb CAB09260 - (295844) opca [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1008, 1025 |
| 3382 | 79241141 (6249, 6250) | Novel Protein sim. GBank gij2131086 emb CAA89409 - (249389) TY4B [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1008, 1017, 1022, 1044 |

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| 3383 | 82361916 (17967, 17968) | Novel Protein sim. GBank g 21312 pir S65270 - CIN2 protein - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1001, 1006, 1008, 1009, 1017, 1022, 1023, 1024, 1026, 1031 |
| 3384 | 79250054 (3947, 3948) | Novel Protein sim. GBank g 2131324 pir S67605 - hypothetical protein YDL070w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1008, 1009, 1023, 1026, 1039, 1044 |
| 3385 | 78700840 (7243, 7244) | Novel Protein sim. GBank g 2131363 pir S67773 - hypothetical protein YDL214c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1017 |
| 3386 | 79612232 (19013, 19014) | Novel Protein sim. GBank g 2131367 pir S67786 - hypothetical protein YDL223c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006, 1024 |
| 3387 | 27966059 (9077, 9078) | Novel Protein sim. GBank g 2131427 pir S59784 - hypothetical protein YDR318w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1034 |
| 3388 | 79224048 (16343, 16344) | Novel Protein sim. GBank g 2131439 pir S70113 - hypothetical protein YDR348c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1034 |
| 3389 | 94127710 (9791, 9792) | Novel Protein sim. GBank g 2131522 pir S69649 - hypothetical protein YDR482c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1019 |
| 3390 | 27843770 (19453, 19454) | Novel Protein sim. GBank g 2131525 pir S69656 - hypothetical protein YDR489w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1006 |
| 3391 | 79601400 (15675, 15676) | Novel Protein sim. GBank g 2131544 pir S69580 - hypothetical protein YDR524c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006 |
| 3392 | 80494094 (17089, 17090) | Novel Protein sim. GBank g 2131759 pir S61623 - hypothetical protein YLR049c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006, 1008, 1012, 1017, 1026, 1034, 1039, 1044 |
| 3393 | 80063200 (14865, 14866) | Novel Protein sim. GBank g 2131774 pir S64929 - hypothetical protein YLR095c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022, 1024, 1039, 1044 |

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| 3394 | 80046588 (10681, 10682) | Novel Protein sim. GBank gi 2132008 pir S66765 - hypothetical protein YOL072w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1024 |
| 3395 | 20699082 (22425, 22426) | Novel Protein sim. GBank gi 2132050 pir S66963 - hypothetical protein YOR080w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006, 1022 |
| 3396 | 78522996 (19713, 19714) | Novel Protein sim. GBank gi 2132053 pir S61651 - hypothetical protein YOR091w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1044 |
| 3397 | 80171188 (9649, 9650) | Novel Protein sim. GBank gi 2132079 pir S67081 - hypothetical protein YOR189w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1026, 1058 |
| 3398 | 80241731 (9467, 9468) | Novel Protein sim. GBank gi 2132083 pir S67089 - hypothetical protein YOR197w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1001, 1003, 1006, 1022, 1044 |
| 3399 | 30664343 (5645, 5646) | Novel Protein sim. GBank gi 2132143 pir S67284 - hypothetical protein YOR372c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 3400 | 16788040 (6009, 6010) | Novel Protein sim. GBank gi 2132211 pir S65168 - hypothetical protein YPL157w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1044 |
| 3401 | 30658468 (17591, 17592) | Novel Protein sim. GBank gi 2132221 pir S65192 - hypothetical protein YPL180w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1026 |
| 3402 | 80216685 (18845, 18846) | Novel Protein sim. GBank gi 2132221 pir S65192 - hypothetical protein YPL180w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1010, 1022, 1023, 1024, 1025, 1034, 1044 |
| 3403 | 94655380 (10543, 10544) | Novel Protein sim. GBank gi 2132225 pir S65212 - hypothetical protein YPL193w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 3404 | 18856013 (9991, 9992) | Novel Protein sim. GBank gi 2132243 pir S61028 - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1024 |
| 3405 | 79415457 (1537, 1538) | Novel Protein sim. GBank gi 2132244 pir S61023 - hypothetical protein YPL242c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006, 1022, 1026 |

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| 3406 | 79862623 (12767, 12768) | Novel Protein sim. GBank gi 2132244 pir S61023 - hypothetical protein YPL242c - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1038 |
| 3407 | 30504759 (3089, 3090) | Novel Protein sim. GBank gi 2132279 pir S69079 - hypothetical protein YPR097w - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1026 |
| 3408 | 29683027 (1093, 1094) | Novel Protein sim. GBank gi 2132286 pir S59777 - hypothetical protein YPR112c - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1009 |
| 3409 | 78487262 (4385, 4386) | Novel Protein sim. GBank gi 2132299 pir S69029 - hypothetical protein YPR140w - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1009 |
| 3410 | 80416610 (10715, 10716) | Novel Protein sim. GBank gi 2132314 pir S59832 - hypothetical protein YPR174c - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1001, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1025, 1026, 1034, 1039, 1044, 1054 |
| 3411 | 79865587 (14455, 14456) | Novel Protein sim. GBank gi 2132314 pir S59832 - hypothetical protein YPR174c - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1038, 1039 |
| 3412 | 11691490 (13615, 13616) | Novel Protein sim. GBank gi 2132443 pir S67691 - probable membrane protein YDL144c - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1034 |
| 3413 | 30245995 (6753, 6754) | Novel Protein sim. GBank gi 2132445 pir S67696 - probable membrane protein YDL148c - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1026 |
| 3414 | 11815275 (803, 804) | Novel Protein sim. GBank gi 2132492 pir S70118 - probable membrane protein YDR288w - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1004 |

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| 3415 | 77518899 (16891, 16892) | Novel Protein sim. GBank gij 2132512 pir S62018 - probable membrane protein YDR539w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1011 |
| 3416 | 78182734 (16523, 16524) | Novel Protein sim. GBank gij 2132645 pir S64754 - probable membrane protein YLL012w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1053 |
| 3417 | 78366762 (19485, 19486) | Novel Protein sim. GBank gij 2132671 pir S61631 - probable membrane protein YLR057w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1008 |
| 3418 | 25316193 (21451, 21452) | Novel Protein sim. GBank gij 2132671 pir S61631 - probable membrane protein YLR057w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1009 |
| 3419 | 80233556 (5185, 5186) | Novel Protein sim. GBank gij 2132679 pir S64916 - probable membrane protein YLR084c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1004, 1006, 1008, 1010, 1017, 1022, 1026, 1044 |
| 3420 | 27931484 (7557, 7558) | Novel Protein sim. GBank gij 2132687 pir S64940 - probable membrane protein YLR104w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006, 1010, 1022 |
| 3421 | 8498667 (21817, 21818) | Novel Protein sim. GBank gij 2132824 pir S68701 - probable membrane protein YOL019w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1034 |
| 3422 | 79608104 (16319, 16320) | Novel Protein sim. GBank gij 2132845 pir S66802 - probable membrane protein YOL106w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1025 |
| 3423 | 16820311 (17299, 17300) | Novel Protein sim. GBank gij 2132852 pir S66835 - probable membrane protein YOL138c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1017 |

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| 3424 | 17938485 (3097, 3098) | Novel Protein sim. GBank gi 2 32868 pir S66936 - probable membrane protein YOR053w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1039 |
| 3425 | 10198761 (13353, 13354) | Novel Protein sim. GBank gi 2 32879 pir S61647 - probable membrane protein YOR086c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003 |
| 3426 | 25335616 (3657, 3658) | Novel Protein sim. GBank gi 2 32889 pir S61667 - probable membrane protein YOR109w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1008 |
| 3427 | 20416759 (14391, 14392) | Novel Protein sim. GBank gi 2 32900 pir S67042 - probable membrane protein YOR154w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004 |
| 3428 | 80234470 (4007, 4008) | Novel Protein sim. GBank gi 2 32906 pir S67067 - probable membrane protein YOR175c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1022, 1023 |
| 3429 | 57530356 (1241, 1242) | Novel Protein sim. GBank gi 2 32917 pir S60941 - probable membrane protein YOR214c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1006, 1008, 1010, 1012, 1022, 1024, 1034, 1039, 1044 |
| 3430 | 27779527 (15327, 15328) | Novel Protein sim. GBank gi 2 32940 pir S67203 - probable membrane protein YOR299w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022, 1024 |
| 3431 | 13526994 (117, 118) | Novel Protein sim. GBank gi 2 32946 pir S58330 - probable membrane protein YOR320c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1024 |
| 3432 | 27788823 (13705, 13706) | Novel Protein sim. GBank gi 2 32947 pir S58333 - probable membrane protein YOR322c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022, 1024 |

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| 3433 | 79452038 (19017, 19018) | Novel Protein sim. GBank gil2133004 pir S65240 - probable membrane protein YPL221w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1008, 1017, 1022, 1023, 1026, 1039 |
| 3434 | 80232215 (323, 324) | Novel Protein sim. GBank gil2133040 pir S59842 - probable membrane protein YPR185w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1009, 1010, 1024 |
| 3435 | 79451977 (4539, 4540) | Novel Protein sim. GBank gil2133040 pir S59842 - probable membrane protein YPR185w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 3436 | 20428628 (13727, 13728) | Novel Protein sim. GBank gil21334419 pir A57075 - tensin - chicken (fragment) | | UNCLASSIFIED | 1010, 1022 |
| 3437 | 65661259 (1723, 1724) | Novel Protein sim. GBank gil2135416 pir 380222 - hypothetical protein - human | | UNCLASSIFIED | 1041 |
| 3438 | 19648067 (5517, 5518) | Novel Protein sim. GBank gil2135416 pir 380222 - hypothetical protein - human | | UNCLASSIFIED | 1017, 1023 |
| 3439 | 20721495 (15509, 15510) | Novel Protein sim. GBank gil2135950 pir S582222 - PQ-rich protein - human | | UNCLASSIFIED | 1006 |
| 3440 | 9945274 (11321, 11322) | Novel Protein sim. GBank gil2137043 pir 468880 - unknown protein - rabbit (fragment) | | UNCLASSIFIED | 1044 |
| 3441 | 20430944 (3251, 3252) | Novel Protein sim. GBank gil2137044 pir 468884 - unknown protein - rabbit (fragment) | | UNCLASSIFIED | 1024 |
| 3442 | 13518144 (9975, 9976) | Novel Protein sim. GBank gil2137044 pir 468884 - unknown protein - rabbit (fragment) | | UNCLASSIFIED | 1024 |
| 3443 | 95199127 (10471, 10472) | Novel Protein sim. GBank gil2137044 pir 468884 - unknown protein - rabbit (fragment) | | UNCLASSIFIED | 1029 |

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| 3444 | 27956156 (5923, 5924) | Novel Protein sim. GBank g 2137729 pir 60167 - regulatory protein Nedd1 - mouse | | UNCLASSIFIED | 1004 |
| 3445 | 86380882 (4425, 4426) | Novel Protein sim. GBank g 2143780 pir 56545 - heparan sulfate proteoglycan - rat | | UNCLASSIFIED | 1053 |
| 3446 | 65376808 (81, 82) | Novel Protein sim. GBank g 2144041 pir 56505 - protein-L-isoadipate(D-aspartate) O-methyltransferase (EC 2.1.1.77) - black rat | | UNCLASSIFIED | 1044 |
| 3447 | 17899265 (17521, 17522) | Novel Protein sim. GBank g 2144188 pir JC4743 - fatty-acid synthase (EC 2.3.1.85) - Mycobacterium tuberculosis | | UNCLASSIFIED | 1044 |
| 3448 | 20625052 (5131, 5132) | Novel Protein sim. GBank g 2145947 pir S72959 - probable integrase - Mycobacterium leprae | | UNCLASSIFIED | 1010 |
| 3449 | 79861915 (4431, 4432) | Novel Protein sim. GBank g 2145957 pir S72983 - probable phosphorylating protein ureC - Mycobacterium leprae | | UNCLASSIFIED | 1012 |
| 3450 | 27843590 (345, 346) | Novel Protein sim. GBank g 2146828 pir S74288 - hypothetical protein YCL008c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 3451 | 78795977 (22439, 22440) | Novel Protein sim. GBank g 2147083 pir S68957 - adhesive protein - Mytilus galloprovincialis | | UNCLASSIFIED | 1026 |
| 3452 | 80503574 (13333, 13334) | Novel Protein sim. GBank g 2181957 emb CAB09445 - (Z236070) hypothetical protein Rv3300c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012 |
| 3453 | 17938994 (15779, 15780) | Novel Protein sim. GBank g 2182006 emb CAB09475 - (Z96072) hypothetical protein Rv2715 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1038 |
| 3454 | 25262844 (1791, 1792) | Novel Protein sim. GBank g 2183273 (AF002133) - MAV266 [Mycobacterium avium] | | UNCLASSIFIED | 1009 |

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| 3455 | 20446782 (8021, 8022) | Novel Protein sim. GBank gi 2190951 (AF002247) - transposase [Rhodococcus erythropolis] | | UNCLASSIFIED | 1024 |
| 3456 | 11091074 (19113, 19114) | Novel Protein sim. GBank gi 2190953 (AF002247) -ORF2 [Rhodococcus erythropolis] | | UNCLASSIFIED | 1006 |
| 3457 | 15015721 (1079, 1080) | Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus] | | UNCLASSIFIED | 1001 |
| 3458 | 99327112 (4143, 4144) | Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus] | | UNCLASSIFIED | 1006, 1010, 1016, 1017, 1022, 1023, 1024, 1029, 1034, 1038, 1039 |
| 3459 | 34129286 (16021, 16022) | Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus] | | UNCLASSIFIED | 1026 |
| 3460 | 79206061 (22517, 22518) | Novel Protein sim. GBank gi 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus] | | UNCLASSIFIED | 1034 |
| 3461 | 57143751 (14417, 14418) | Novel Protein sim. GBank gi 2197106 (AF003693) - scaffold protein Pbp1 homolog [Mus musculus] | | UNCLASSIFIED | 1022, 1034, 1058 |
| 3462 | 78471189 (13205, 13206) | Novel Protein sim. GBank gi 2204224 emb CAA74161 - (Y13849) alpha-galactosidase [Hordeum vulgare] | | UNCLASSIFIED | 1053 |
| 3463 | 13502091 (20483, 20484) | Novel Protein sim. GBank gi 221352 emb CAB09730 - (Z97050) hypothetical protein Rv0190 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1027 |
| 3464 | 80048915 (8137, 8138) | Novel Protein sim. GBank gi 2218156 (AF005091) - lipase/esterase; Ester [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1034 |
| 3465 | 30621011 (12939, 12940) | Novel Protein sim. GBank gi 2224529 dbj BAA20754 - (AB002292) KIAA0294 [Homo sapiens] | | UNCLASSIFIED | 1026 |

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| 3466 | 27966891 (1313, 1314) | Novel Protein sim. GBank gil2224589 dbj BAA20782 - (AB002322) | | | |
| 3467 | 56713726 (4267, 4268) | Novel Protein sim. GBank gil2225877 dbj BAA20875.1 - (AB002406) TIP49 [Rattus norvegicus] | | UNCLASSIFIED | 1016 |
| 3468 | 207080807 (20953, 20954) | Novel Protein sim. GBank gil2225941 emb CAA69714 - (Y08460) Mdes protein [Mus musculus] | | UNCLASSIFIED | 1022, 1034 |
| 3469 | 37374805 (10051, 10052) | Novel Protein sim. GBank gil2226241 emb CAA74493.1 - (Y14082) hypothetical protein [Bacillus subtilis] | | UNCLASSIFIED | 1023 |
| 3470 | 79553182 (12831, 12832) | Novel Protein sim. GBank gil2226238 emb CAA74526.1 - (Y14083) hypothetical protein [Bacillus subtilis] | | UNCLASSIFIED | 1039 |
| 3471 | 80026633 (9661, 9662) | Novel Protein sim. GBank gil2226243 emb CAA74531.1 - (Y14083) hypothetical protein [Bacillus subtilis] | | UNCLASSIFIED | 1006 |
| 3472 | 77516818 (20355, 20356) | Novel Protein sim. GBank gil2226283 (U70063) - GumP [Xanthomonas campestris] | | UNCLASSIFIED | 1049 |
| 3473 | 29247926 (7377, 7378) | Novel Protein sim. GBank gil2239238 emb CAB10154 - (Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1022 |
| 3474 | 21425340 (3577, 3578) | Novel Protein sim. GBank gil22446527 dbj BAA21097 - (D89876) hemolysin [Edwardsiella tarda] | | UNCLASSIFIED | 1053 |
| 3475 | 36999858 (11821, 11822) | Novel Protein sim. GBank gil2253084 emb CAA74602 - (Y14206) orfsyn [Streptomyces coelicolor] | | UNCLASSIFIED | 1001 |
| 3476 | 23308531 (14629, 14630) | Novel Protein sim. GBank gil2262102 gb AAB63610.1 - (AC002343) hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1053 |
| 3477 | 78520830 (11081, 11082) | Novel Protein sim. GBank gil226591 prf 1603236B - ATP synthase 18kD-like protein 4 [Saccharomyceles cerevisiae] | | UNCLASSIFIED | 1009 |

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| 3478 | 20739345 (3283, 3284) | Novel Protein sim. GBank gi 226743 pf1 1604369A - sulfated surface glycoprotein SSG185 [Volvox carterii] | | UNCLASSIFIED | 1022 |
| 3479 | 36996952 (8143, 8144) | Novel Protein sim. GBank gi 2270983 (U90220) - orf3 [Sinorhizobium meliloti] | | UNCLASSIFIED | 1001 |
| 3480 | 23333109 (4883, 4884) | Novel Protein sim. GBank gi 2275199 (AC002337) - hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1053 |
| 3481 | 8498660 (21299, 21300) | Novel Protein sim. GBank gi 2276127 dbj BAA21556 - (D88585), hepatitis A virus receptor [Chlorocebus aethiops] | | UNCLASSIFIED | 1024 |
| 3482 | 11817991 (21249, 21250) | Novel Protein sim. GBank gi 2276392 (U02634) - DbxR/iron regulated protein 2 [Corynebacterium diphtheriae] | | UNCLASSIFIED | 1004 |
| 3483 | 30750523 (18449, 18450) | Novel Protein sim. GBank gi 2282048 (AF009900) - Z223 protein [Vibrio shiloi] | | UNCLASSIFIED | 1023 |
| 3484 | 9857085 (15293, 15294) | Novel Protein sim. GBank gi 2288879 emb CAA1776 - (Y10817) molybdate-binding periplasmic protein [Athrobacter nicotinovorans] | | UNCLASSIFIED | 1008 |
| 3485 | 37032756 (7041, 7042) | Novel Protein sim. GBank gi 2290990 (AF006000) - Brg1 [Brachetella pertussis] | | UNCLASSIFIED | 1038 |
| 3486 | 37028591 (15467, 15468) | Novel Protein sim. GBank gi 2290990 (AF006000) - Brg1 [Brachetella pertussis] | | UNCLASSIFIED | 1038 |
| 3487 | 13076276 (5581, 5582) | Novel Protein sim. GBank gi 2292957 emb CAB10899 - (Z98209) hypothetical protein Rv2723 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1031 |
| 3488 | 27981617 (14005, 14006) | Novel Protein sim. GBank gi 2292959 emb CAB10901 - (Z98209) hflX [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1006 |
| 3489 | 29518763 (2949, 2950) | Novel Protein sim. GBank gi 2293166 (AF008220) - amino acid transporter [Bacillus subtilis] | | UNCLASSIFIED | 1016 |
| 3490 | 78760637 (1991, 1992) | Novel Protein sim. GBank gi 2293167 (AF008220) - probable lysophospholipase [Bacillus subtilis] | | UNCLASSIFIED | 1003 |

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| 3491 | 11289499 (18353, 18354) | Novel Protein sim. GBank gil2293174 (AF008220) - YtfF [Bacillus subtilis] | | UNCLASSIFIED | 1022 |
| 3492 | 78675833 (21063, 21064) | Novel Protein sim. GBank gil2293568 (AF012897) - HvB12D homolog [Oryza sativa] | | UNCLASSIFIED | 1017 |
| 3493 | 13886343 (4129, 4130) | Novel Protein sim. GBank gil2313702[gb]AAD07650_11 - (AE000571) H. pylori predicted coding region HP0578 [Helicobacter pylori 26695] | | UNCLASSIFIED | 1053 |
| 3494 | 79247119 (12493, 12494) | Novel Protein sim. GBank gil2314191[gb]AAD08089_11 - (AE000612) conserved hypothetical integral membrane protein [Helicobacter pylori 26695] | | UNCLASSIFIED | 1038 |
| 3495 | 80209505 (15055, 15056) | Novel Protein sim. GBank gil2314238[gb]AAD08133_11 - (AE000615) H. pylori predicted coding region HP1081 [Helicobacter pylori 26695] | | UNCLASSIFIED | 1034 |
| 3496 | 13883844 (16667, 16668) | Novel Protein sim. GBank gil2314367[gb]AAD08251_11 - (AE000626) multidrug resistance protein (hda) [Helicobacter pylori 26695] | | UNCLASSIFIED | 1053 |
| 3497 | 8975576 (3615, 3616) | Novel Protein sim. GBank gil231481[sp]P29858 AAC_ACTUT - ACULEACIN AACYLASE PRECURSOR | | UNCLASSIFIED | 1017 |
| 3498 | 20634331 (17073, 17074) | Novel Protein sim. GBank gil2317934 (U97553) - unknown [murine herpesvirus 68] | | UNCLASSIFIED | 1004 |
| 3499 | 214117200 (16249, 16250) | Novel Protein sim. GBank gil232042[sp]P29541 EFG_STRRA - ELONGATION FACTOR G (EF-G) | | UNCLASSIFIED | 1022 |
| 3500 | 20282053 (6479, 6480) | Novel Protein sim. GBank gil2326732[emb]CAB10946I - (Z98268) tyrS [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1022 |
| 3501 | 11347016 (17377, 17378) | Novel Protein sim. GBank gil2326732[emb]CAB10946I - (Z98268) tyrS [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1034 |
| 3502 | 80050106 (19247, 19248) | Novel Protein sim. GBank gil2326739[emb]CAB10953I - (Z98268) recN [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1004, 1006, 1022, 1044 |

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| 3503 | 79825231 (2713, 2714) | Novel Protein sim. GBank gi 2326740 emb CAB10954 - (Z98268) hypothetical protein Rv1697 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1039 |
| 3504 | 80092742 (6719, 6720) | Novel Protein sim. GBank gi 2330641 emb CAA74897 - (Y14568) htrB [Pseudomonas fluorescens] | UNCLASSIFIED | 1006 |
| 3505 | 80239603 (18457, 18458) | Novel Protein sim. GBank gi 2330791 emb CAB11265 - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe] | UNCLASSIFIED | 1004, 1010 |
| 3506 | 20288157 (1181, 1182) | Novel Protein sim. GBank gi 2337823 emb CAB11300 - (Z98604) hypothetical protein MLCB2052.02 [Mycobacterium leprae] | UNCLASSIFIED | 1034 |
| 3507 | 85800430 (9741, 9742) | Novel Protein sim. GBank gi 2337836 emb CAB11328 - (Z98604) ABC-type sugar transport protein [Mycobacterium leprae] | UNCLASSIFIED | 1025 |
| 3508 | 23302830 (9383, 9384) | Novel Protein sim. GBank gi 2340008 emb CAB11358 - (Z98682) YblL protein [Bacillus subtilis] | UNCLASSIFIED | 1008 |
| 3509 | 79249087 (19971, 19972) | Novel Protein sim. GBank gi 2342651 emb CAB11373 - (Z98741) nicotinate- nucleotide -dimethylbenzimidazole phosphoribosyltransferase [Mycobacterium leprae] | UNCLASSIFIED | 1024, 1044 |
| 3510 | 11751284 (1269, 1270) | Novel Protein sim. GBank gi 2343283 (AF015297) - IE2 hom [Human herpesvirus 6 (strain Uganda- 1102)] | UNCLASSIFIED | 1022 |
| 3511 | 80170492 (9687, 9688) | Novel Protein sim. GBank gi 2347197 (AC002338) - hypothetical protein [Arabidopsis thaliana] | UNCLASSIFIED | 1008, 1058 |
| 3512 | 70074365 (5251, 5252) | Novel Protein sim. GBank gi 2351772 (U90267) p39 [Mus musculus] | UNCLASSIFIED | 1042 |

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| 3513 | 27365977 (15743) 15744) | Novel Protein sim. GBank gj 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus] | | UNCLASSIFIED | 1022 |
| 3514 | 9666959 (19727, 19728) | Novel Protein sim. GBank gj 2370322 emb CAB11595 - (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1023 |
| 3515 | 20485309 (9979, 9980) | Novel Protein sim. GBank gj 2384728 gb AAB69862.1 - (AF015883) hydroxyproline-rich glycoprotein gas28p precursor [Chlamydomonas reinhardtii] | | UNCLASSIFIED | 1022 |
| 3516 | 94140178 (5271, 5272) | Novel Protein sim. GBank gj 238898 emb CAB11718 - (Z98980) actin associated protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1003, 1010, 1018, 1023, 1038, 1049, 1054 |
| 3517 | 11091025 (13033, 13034) | Novel Protein sim. GBank gj 2398732 emb CAA60713 - (X87256) glutamine amidotransferase [Rhodobacter sphaeroides] | | UNCLASSIFIED | 1006 |
| 3518 | 19888230 (13891, 13892) | Novel Protein sim. GBank gj 2407197 (AF07138) - cob(I)alamin adenosyltransferase [Rhodobacter capsulatus] | | UNCLASSIFIED | 1034 |
| 3519 | 95005613 (12071, 12072) | Novel Protein sim. GBank gj 2414562 emb CAB16451 - (Z99263) polyphosphate kinase [Mycobacterium leprae] - | | UNCLASSIFIED | 1034 |
| 3520 | 13085228 (20019, 20020) | Novel Protein sim. GBank gj 2415403 (AF015775) - acetylornithine deacetylase [Bacillus subtilis] | | UNCLASSIFIED | 1027 |
| 3521 | 9383239 (3637, 3638) | Novel Protein sim. GBank gj 2415704 emb CAA04698 - (AJ001361) proline iminopeptidase [Propionibacterium freudenreichii subsp. <i>shermanii</i>] | | UNCLASSIFIED | 1017 |
| 3522 | 10886132 (4323, 4324) | Novel Protein sim. GBank gj 2435511 (AF024504) - contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis italiana] | | UNCLASSIFIED | 1031 |

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| 3523 | 78936412 (8079, 8080) | Novel Protein sim. GBank gi 2435511 (AF024504) - contains similarity to proly 4-hydroxylase alpha subunit [Arabidopsis thaliana] | | UNCLASSIFIED | 1008, 1044 |
| 3524 | 20616812 (13419, 13420) | Novel Protein sim. GBank gi 2440103 emb CAB16676 - (Z99494) hypothetical protein M/LCB57_36c [Mycobacterium leprae] | | UNCLASSIFIED | 1010 |
| 3525 | 27969777 (18557, 18558) | Novel Protein sim. GBank gi 2444666 (AF021840) - Aida [Ralstonia solanacearum] | | UNCLASSIFIED | 1022 |
| 3526 | 52563365 (16179, 16180) | Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens] | | UNCLASSIFIED | 1039 |
| 3527 | 11706354 (19055, 19056) | Novel Protein sim. GBank gi 2492593 spi P55604 Y4OS_RHISN - PROBABLE ABC TRANSPORTER ATP-BINDING PROTEIN Y4OS | | UNCLASSIFIED | 1022 |
| 3528 | 56288155 (6989, 6990) | Novel Protein sim. GBank gi 2493240 isp O10341 Y091_NPVOP - HYPOTHETICAL 29.3 KD PROTEIN (ORF52) | | UNCLASSIFIED | 1037, 1038 |
| 3529 | 39581745 (15797, 15798) | Novel Protein sim. GBank gi 2493240 isp O10341 Y091_NPVOP - HYPOTHETICAL 29.3 KD PROTEIN (ORF52) | | UNCLASSIFIED | 1038 |
| 3530 | 79637559 (2301, 2302) | Novel Protein sim. GBank gi 2494014 isp Q59967 SRPH_SYNPT - SERINE ACETYLTRANSFERASE, PLASMID (SAT) | | UNCLASSIFIED | 1006, 1038 |
| 3531 | 80051091 (9435, 9436) | Novel Protein sim. GBank gi 2494531 isp P75938 FLGF_ECOLI - FLAGELLAR BASAL-BODY ROD PROTEIN FLGF (PUTATIVE PROXIMAL ROD PROTEIN) | | UNCLASSIFIED | 1004 |
| 3532 | 32153325 (17829, 17830) | Novel Protein sim. GBank gi 2494531 isp Q52950 FLGH_RHIME - FLAGELLAR L-RING PROTEIN PRECURSOR (BASAL BODY L-RING PROTEIN) | | UNCLASSIFIED | 1023 |

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| 3533 | 86380254 (4415, 4416) | Novel Protein sim. GBank gi 2494630 sp Q64467 G3PT_MOUSE - GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-SPECIFIC (GAPDH) | UNCLASSIFIED | 1053 |
| 3534 | 20724433 (15979, 15980) | Novel Protein sim. GBank gi 2495561 sp P77300 YAGL_ECOLI - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PERR-ARGF INTERGENIC REGION | UNCLASSIFIED | 1006 |
| 3535 | 12917471 (9881, 9882) | Novel Protein sim. GBank gi 2495562 sp P77239 YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRRB-PHEP INTERGENIC REGION PRECURSOR | UNCLASSIFIED | 1004 |
| 3536 | 27972911 (18581, 18582) | Novel Protein sim. GBank gi 2495572 sp P7744 YBGJ_ECOLI - HYPOTHETICAL 23.9 KD PROTEIN IN PHRB-NEI INTERGENIC REGION | UNCLASSIFIED | 1053 |
| 3537 | 11777222 (15459, 15460) | Novel Protein sim. GBank gi 2495597 sp P77334 YCIR_ECOLI - HYPOTHETICAL 74.7 KD PROTEIN IN PHRB-RNB INTERGENIC REGION | UNCLASSIFIED | 1022 |
| 3538 | 80248157 (16699, 16700) | Novel Protein sim. GBank gi 2495634 sp P77651 8 YFDE_ECOLI - HYPOTHETICAL 43.3 KD PROTEIN IN EVGS-GLK INTERGENIC REGION | UNCLASSIFIED | 1003, 1006 |
| 3539 | 79872214 (3367, 3368) | Novel Protein sim. GBank gi 2495648 sp P76562 YPF1_ECOLI - HYPOTHETICAL 74.9 KD PROTEIN IN DAPE-PURC INTERGENIC REGION | UNCLASSIFIED | 1017 |
| 3540 | 20614013 (14781, 14782) | Novel Protein sim. GBank gi 2495651 sp P55734 YGAP_ECOLI - HYPOTHETICAL 18.6 KD PROTEIN IN GABP-STPA INTERGENIC REGION | UNCLASSIFIED | 1010 |
| 3541 | 11130950 (7313, 7314) | Novel Protein sim. GBank gi 2495685 sp Q57498 YA53_HAEIN - HYPOTHETICAL PROTEIN_H1053 | UNCLASSIFIED | 1004 |

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| 3542 | 27794695 (15277) 15278) | Novel Protein sim. GBank gi 2495701 sp Q14135 Y121_HUMAN - HYPOTHETICAL PROTEIN KIAA0121 | | UNCLASSIFIED | 1024 |
| 3543 | 78377579 (2521, 2522) | Novel Protein sim. GBank gi 2496136 sp Q58288 Y878_METJA - HYPOTHETICAL PROTEIN MJ0878 | | UNCLASSIFIED | 1008, 1016, 1026 |
| 3544 | 80248456 (1931, 1932) | Novel Protein sim. GBank gi 2496481 sp Q50724 Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C | | UNCLASSIFIED | 1006, 1010, 1022, 1023, 1024, 1026, 1031, 1034, 1039 |
| 3545 | 78461809 (2507, 2508) | Novel Protein sim. GBank gi 2496484 sp Q49741 Y09T_MYCTU - HYPOTHETICAL 28.6 KD PROTEIN B1620_F3_119 | | UNCLASSIFIED | 1023, 1049 |
| 3546 | 78490684 (6681, 6682) | Novel Protein sim. GBank gi 2496491 sp Q50739 Y0A9_MYCTU - HYPOTHETICAL 47.5 KD PROTEIN CY9C4.09 | | UNCLASSIFIED | 1030 |
| 3547 | 79641125 (21033, 21034) | Novel Protein sim. GBank gi 2496533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08 | | UNCLASSIFIED | 1039 |
| 3548 | 11360207 (2209, 2210) | Novel Protein sim. GBank gi 2496621 sp P55441 Y4FC_RHISN - HYPOTHETICAL MONOOXYGENASE Y4FC | | UNCLASSIFIED | 1006 |
| 3549 | 80081058 (19623, 19624) | Novel Protein sim. GBank gi 2496798 sp P74311 Y944_SYNY3 - HYPOTHETICAL 42.4 KD PROTEIN SLR0944 | | UNCLASSIFIED | 1017, 1034 |
| 3550 | 66137941 (20945, 20946) | Novel Protein sim. GBank gi 2496821 sp Q11116 YX0A_CAEEL - HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X | | UNCLASSIFIED | 1003 |
| 3551 | 8488862 (21215, 21216) | Novel Protein sim. GBank gi 2497058 sp Q03102 YMN1_YEAST - HYPOTHETICAL 40.0 KD PROTEIN IN COX14 5 REGION | | UNCLASSIFIED | 1022 |

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| 3552 | 27338700 (22901, 22902) | Novel Protein sim. GBank gi 2497061 sp Q03124 YMM7 YEAST - HYPOTHETICAL 65.2 KD PROTEIN IN COX14- HMGS INTERGENIC REGION | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1034 |
| 3553 | 80221866 (6975, 6976) | Novel Protein sim. GBank gi 2497090 sp Q04693 YME9 YEAST - HYPOTHETICAL 153.8 KD PROTEIN IN GAL80- PRP39 INTERGENIC REGION | UNCLASSIFIED | 1004, 1006, 1009, 1010, 1012, 1016, 1023, 1024, 1034, 1038, 1044 |
| 3554 | 80233217 (14689, 14690) | Novel Protein sim. GBank gi 2497090 sp Q04693 YME9 YEAST - HYPOTHETICAL 153.8 KD PROTEIN IN GAL80- PRP39 INTERGENIC REGION | UNCLASSIFIED | 1004, 1006, 1009, 1010, 1016, 1017, 1022, 1025, 1026, 1038, 1039 |
| 3555 | 32124806 (20505, 20506) | Novel Protein sim. GBank gi 2497099 sp Q03712 YMD3 YEAST - HYPOTHETICAL 17.7 KD PROTEIN IN AMD1- RAD52 INTERGENIC REGION | UNCLASSIFIED | 1003, 1004, 1006, 1009, 1012, 1017, 1022, 1038, 1044 |
| 3556 | 28987444 (22625, 22626) | Novel Protein sim. GBank gi 2497112 sp Q03667 YMO2 YEAST - HYPOTHETICAL 16.7 KD PROTEIN IN CDC5- MVP1 INTERGENIC REGION | UNCLASSIFIED | 1023, 1024 |
| 3557 | 5641214 (17489, 17490) | Novel Protein sim. GBank gi 2497143 sp Q04279 YMX8 YEAST - HYPOTHETICAL 105.9 KD PROTEIN IN ADH3- RCA1 INTERGENIC REGION | UNCLASSIFIED | 1058 |
| 3558 | 78729015 (19393, 19394) | Novel Protein sim. GBank gi 2497148 sp Q03153 YY8 YEAST - HYPOTHETICAL 70.4 KD PROTEIN IN SNZ1- YPK2 INTERGENIC REGION | UNCLASSIFIED | 1008 |
| 3559 | 80218584 (2733, 2734) | Novel Protein sim. GBank gi 2497157 sp Q03879 YMO9 YEAST - VERY HYPOTHETICAL 14.1 KD PROTEIN IN RPL10B- GCR3 INTERGENIC REGION | UNCLASSIFIED | 1003, 1022 |

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| 3560 | 78971625 (7787, 7788) | Novel Protein sim. GBank gi 2497271 sp Q03264 YM8O YEAST - HYPOTHETICAL 59.5 KD PROTEIN IN HDF1- MRPL33 INTERGENIC REGION | UNCLASSIFIED | 1017 |
| 3561 | 29346175 (17229, 17230) | Novel Protein sim. GBank gi 2497226 sp Q04869 YM94 YEAST - HYPOTHETICAL 38.2 KD PROTEIN IN PRE5- FET4 INTERGENIC REGION | UNCLASSIFIED | 1022 |
| 3562 | 5715218 (867, 868) | Novel Protein sim. GBank gi 2497227 sp Q04893 YM96 YEAST - HYPOTHETICAL 113.1 KD PROTEIN IN PRE5- FET4 INTERGENIC REGION | UNCLASSIFIED | 1058 |
| 3563 | 79821196 (11795, 11796) | Novel Protein sim. GBank gi 2497384 sp Q46087 TRAT_CHEHE - TRANSPOSEASE | UNCLASSIFIED | 1039 |
| 3564 | 20399484 (6139, 6140) | Novel Protein sim. GBank gi 2497419 sp P55635 Y4RB_RHISN - PUTATIVE INTEGRASE/RECOMBINASE_Y4RB | UNCLASSIFIED | 1004 |
| 3565 | 14218558 (6293, 6294) | Novel Protein sim. GBank gi 2497171 sp P55689 HPA0 HELPY - NEURAMINYLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N- ACETYLNEURAMINYLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR- BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN) | UNCLASSIFIED | 1053 |
| 3566 | 78461564 (9069, 9070) | Novel Protein sim. GBank gi 2498270 sp Q02534 CUS1 YEAST - CUS1 PROTEIN | UNCLASSIFIED | 1006, 1044 |
| 3567 | 21145908 (16663, 16664) | Novel Protein sim. GBank gi 2499125 sp Q07818 VP13 YEAST - VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13 | UNCLASSIFIED | 1058 |

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| 3568 | 80190320 (18657, 18658) | Novel Protein sim. GBank gi 2498125 sp Q07878 YP13_YEAST - VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13 | UNCLASSIFIED | 1058 |
| 3569 | 16332986 (13881, 13882) | Novel Protein sim. GBank gi 2499516 sp Q57290 Y740_HAEIN - PROBABLE PHOSPHOMANNONOUTASE (PMM) | UNCLASSIFIED | 1024 |
| 3570 | 12936190 (15989, 15990) | Novel Protein sim. GBank gi 2500021 sp Q46480 PUR9_CHRV1 - PHOSPHORIBOSYLAMINOIMIDAZOLECARBOX AMIDE FORMYLTRANSFERASE (AICAR TRANSFORMYLASE) / IMP CYCLOHYDROLASE (INOSINICASE) (IMP SYNTHETASE) (ATIC) | UNCLASSIFIED | 1004 |
| 3571 | 27972399 (12581, 12582) | Novel Protein sim. GBank gi 2500034 sp P72170 PYRC_PSEAE - DIHYDROOROTASE (DHOASE) | UNCLASSIFIED | 1022 |
| 3572 | 80054174 (10931, 10932) | Novel Protein sim. GBank gi 2500056 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME | UNCLASSIFIED | 1004 |
| 3573 | 20726654 (13265, 13266) | Novel Protein sim. GBank gi 2500056 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME | UNCLASSIFIED | 1006 |
| 3574 | 11102137 (5021, 5022) | Novel Protein sim. GBank gi 2500728 sp Q59912 SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT | UNCLASSIFIED | 1006 |
| 3575 | 77600954 (21265, 21266) | Novel Protein sim. GBank gi 2500739 sp Q51455 CHEY_PSEAE - CHEMOTAXIS PROTEIN CHEY | UNCLASSIFIED | 1049 |
| 3576 | 78674837 (14837, 14838) | Novel Protein sim. GBank gi 2500772 sp Q07657 YD25_YEAST - HYPOTHETICAL 62.6 KD PROTEIN IN CDC13-GCS1 INTERGENIC REGION | UNCLASSIFIED | 1017 |

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| 3577 | 11392472 (10613, 10614) | Novel Protein sim. GBank gi 2500985 sp Q55690 SYGB_ SYNY3 - GLYCYL- TRNA SYNTHETASE BETA CHAIN (GLYCINE- TRNA LIGASE BETA CHAIN) (GLYRS) | UNCLASSIFIED | 1024 |
| 3578 | 20263972 (1027, 1028) | Novel Protein sim. GBank gi 2501000 sp Q50641 SYH_MYCTU - HISTIDYL- TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS) | UNCLASSIFIED | 1034 |
| 3579 | 79631866 (995, 996) | Novel Protein sim. GBank gi 2501027 sp P71698 SYL_MYCTU - LEUCYL- TRNA SYNTHETASE (LEUCINE-TRNA LIGASE) (LEURS) | UNCLASSIFIED | 1039 |
| 3580 | 25321667 (18609, 18610) | Novel Protein sim. GBank gi 2501040 sp Q005814 SYP_MYCTU - PROLYL- TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS) | UNCLASSIFIED | 1008 |
| 3581 | 27837378 (10319, 10320) | Novel Protein sim. GBank gi 2501048 sp Q55486 SYR_SYNY3 - ARGINYL- TRNA SYNTHETASE (ARGININE-TRNA LIGASE) (ARGRS) | UNCLASSIFIED | 1024, 1034 |
| 3582 | 80050861 (7189, 7190) | Novel Protein sim. GBank gi 2501051 sp Q05506 SYRC_YEAST - PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (ARGININE-TRNA LIGASE)- (ARGRS) | UNCLASSIFIED | 1034 |
| 3583 | 11759455 (22289, 22290) | Novel Protein sim. GBank gi 2501062 sp Q55886 SYT_SYNY3 - THREONYL- TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS) | UNCLASSIFIED | 1024 |
| 3584 | 91213847 (15803, 15804) | Novel Protein sim. GBank gi 2501068 sp Q58413 SYV_METJA - VALYL- TRNA SYNTHETASE (VALINE-TRNA LIGASE) (VALRS) | UNCLASSIFIED | 1008, 1024, 1029 |

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| 3585 | 20451598 (12643, 12644) | Novel Protein sim. GBank gi 2501069 sp Q46127 SYW_CLOLO-TRYPTOPHANYL-TRNA SYNTETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS) | | UNCLASSIFIED | 1024 |
| 3586 | 80049352 (22959, 22960) | Novel Protein sim. GBank gi 2501071 sp Q49901 SYW_MYCLE-TRYPTOPHANYL-TRNA SYNTETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS) | | UNCLASSIFIED | 1010, 1024 |
| 3587 | 79411738 (3153, 3154) | Novel Protein sim. GBank gi 25014371 sp Q06624 RH31_YEAST - DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG) | | UNCLASSIFIED | 1010 |
| 3588 | 25259471 (9337, 9338) | Novel Protein sim. GBank gi 2501527 sp P77338 AEFA_ECOLI - AEFA PROTEIN | | UNCLASSIFIED | 1008, 1017 |
| 3589 | 94141264 (21, 22) | Novel Protein sim. GBank gi 2501557 sp Q47679 YAFV_ECOLI - HYPOTHETICAL 28.9 KD PROTEIN IN DNAQ-GMHA INTERGENIC REGION | | UNCLASSIFIED | 1010 |
| 3590 | 27847764 (11175, 11176) | Novel Protein sim. GBank gi 2501612 sp Q08960 YP07_YEAST - HYPOTHETICAL 89.8 KD PROTEIN YPL207W | | UNCLASSIFIED | 1010 |
| 3591 | 78678606 (7485, 7486) | Novel Protein sim. GBank gi 2501652 sp Q47755 DINP_ECOLI - DNA-DAMAGE-INDUCIBLE PROTEIN P | | UNCLASSIFIED | 1017 |
| 3592 | 37034484 (22781, 22782) | Novel Protein sim. GBank gi 2501679 sp Q45826 YMDA_CHLAU - HYPOTHETICAL PROTEIN IN MDH 5' REGION (ORFA) | | UNCLASSIFIED | 1012 |
| 3593 | 81815581 (12125, 12126) | Novel Protein sim. GBank gi 2506592 sp P45568 DXR_ECOLI - 1-DEOXY-D-XYULLOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP REDUCTOISOMERASE) | | UNCLASSIFIED | 1054 |

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| 3594 | 79769352 (14307, 14308) | Novel Protein sim. GBank gi 2506652 sp P45576 YCM_ECOLI - HYPOTHETICAL 44.5 KD PROTEIN IN PGPB-PYRF INTERGENIC REGION PRECURSOR | | UNCLASSIFIED | 1010, 1023 |
| 3595 | 78913745 (8093, 8094) | Novel Protein sim. GBank gi 2506664 sp P40120 YDCG_ECOLI - 59.4 PROTEIN IN TRG-RM1 INTERGENIC REGION PRECURSOR | | UNCLASSIFIED | 1039 |
| 3596 | 20747431 (12545, 12546) | Novel Protein sim. GBank gi 2506664 sp P40120 YDCG_ECOLI - 59.4 PROTEIN IN TRG-RM1 INTERGENIC REGION PRECURSOR | | UNCLASSIFIED | 1022 |
| 3597 | 20433662 (15745, 15746) | Novel Protein sim. GBank gi 2506668 sp P31122 YDEA_ECOLI - HYPOTHETICAL 42.5 KD PROTEIN IN UXAB-MARR INTERGENIC REGION | | UNCLASSIFIED | 1024 |
| 3598 | 79239991 (8229, 8230) | Novel Protein sim. GBank gi 2506685 sp P38097 YEGE_ECOLI - HYPOTHETICAL 123.9 KD PROTEIN IN UDK-ALKA INTERGENIC REGION | | UNCLASSIFIED | 1039 |
| 3599 | 11768047 (4225, 4226) | Novel Protein sim. GBank gi 2506697 sp P46490 YFCA_HAEIN - HYPOTHETICAL PROTEIN_HI0198 | | UNCLASSIFIED | 1022 |
| 3600 | 10372158 (13799, 13800) | Novel Protein sim. GBank gi 2506712 sp P37350 YGDH_ECOLI - HYPOTHETICAL 51.0 KD PROTEIN IN BARA-SDAC INTERGENIC REGION | | UNCLASSIFIED | 1044 |
| 3601 | 20429935 (17113, 17114) | Novel Protein sim. GBank gi 2507089 sp P31554 OSTA_ECOLI - ORGANIC SOLVENT TOLERANCE PROTEIN PRECURSOR | | UNCLASSIFIED | 1010 |
| 3602 | 80499554 (22967, 22968) | Novel Protein sim. GBank gi 2507128 sp Q03336 SM30_RAT - SENESCEENCE MARKER PROTEIN-30 (SMP-30) (REGUCALCIN) (RC) | | UNCLASSIFIED | 1012 |

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| 3603 | 20177101 (17499, 17500) | Novel Protein sim. GBank gi 2507435 sp P07813 SYL_ECOLI - LEUCYL-TRNA SYNTHETASE (LEUCINE--tRNA LIGASE) (LEURS) | | UNCLASSIFIED | 1010 |
| 3604 | 80027060 (15023, 15024) | Novel Protein sim. GBank gi 2507450 sp P43531 YNFM_ECOLI - HYPOTHETICAL 45.3 KD PROTEIN IN MUC-ASR INTERGENIC REGION | | UNCLASSIFIED | 1003, 1006, 1009, 1023, 1024, 1054 |
| 3605 | 28455892 (17853, 17854) | Novel Protein sim. GBank gi 2565334 (AF026066) - sulfite reductase [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1003 |
| 3606 | 86380010 (4081, 4082) | Novel Protein sim. GBank gi 2576345 (AC002400) - Acyl carrier protein, Mitochondrial (ACP) [5 partial] [Homo sapiens] | | UNCLASSIFIED | 1053 |
| 3607 | 17892336 (5607, 5608) | Novel Protein sim. GBank gi 2578384 emb CAA15469 - (AL008609) glycine cleavage system h protein [Mycobacterium leprae] | | UNCLASSIFIED | 1039 |
| 3608 | 11419478 (20695, 20696) | Novel Protein sim. GBank gi 2582195 (AF017444) - NADP-dependent malic enzyme; TME [Sinorhizobium meliloti] | | UNCLASSIFIED | 1017 |
| 3609 | 144011728 (6331, 6332) | Novel Protein sim. GBank gi 2584886 (AF020706) - methylase Hpy1 [Helicobacter pylori] | | UNCLASSIFIED | 1053 |
| 3610 | 80059383 (1257, 1258) | Novel Protein sim. GBank gi 2612814 emb CAA15531 - (AL008883) hypothetical protein Rv2869c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012, 1024 |
| 3611 | 25259035 (6957, 6958) | Novel Protein sim. GBank gi 2612814 emb CAA15531 - (AL008883) hypothetical protein Rv2869c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1026 |
| 3612 | 65488385 (5181, 5182) | Novel Protein sim. GBank gi 2621621 (AE000837) - cationic amino acid transporter related protein [Methanobacterium thermoautotrophicum] | | UNCLASSIFIED | 1023 |

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| 3613 | 65688850 (22599, 22600) | Novel Protein sim. GBank gi 2622301 (AE000887) - transcriptional regulator [Methanobacterium thermoautotrophicum] | | UNCLASSIFIED | 1041 |
| 3614 | 77520851 (12163, 12164) | Novel Protein sim. GBank gi 2622544 (AE000905) - branched-chain amino-acid aminotransferase [Methanobacterium thermoautotrophicum] | | UNCLASSIFIED | 1049 |
| 3615 | 66490085 (10173, 10174) | Novel Protein sim. GBank gi 2622939 (AE000934) - phytoene dehydrogenase [Methanobacterium thermoautotrophicum] | | UNCLASSIFIED | 1029 |
| 3616 | 2028991 (433, 434) | Novel Protein sim. GBank gi 2624270 emb CAA15544 - (AL008967) ftsK [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1034 |
| 3617 | 79564053 (4517, 4518) | Novel Protein sim. GBank gi 26268331dbj BAA23410 - (D86947) chemotactic transducer [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1017 |
| 3618 | 85518302 (7081, 7082) | Novel Protein sim. GBank gi 2632048 emb CAA05607 - (AJ002571) YkoJ [Bacillus subtilis] | | UNCLASSIFIED | 1049 |
| 3619 | 20446754 (2043, 2044) | Novel Protein sim. GBank gi 2652362 emb CAB11871 - (Z99104) similar to hypothetical proteins [Bacillus subtilis] | | UNCLASSIFIED | 1024 |
| 3620 | 20297916 (16529, 16530) | Novel Protein sim. GBank gi 2632999 emb CAB12505 - (Z99107) similar to hypothetical proteins [Bacillus subtilis] | | UNCLASSIFIED | 1034 |
| 3621 | 20456427 (12383, 12384) | Novel Protein sim. GBank gi 2633557 emb CAB13060 - (Z99110) yidF [Bacillus subtilis] | | UNCLASSIFIED | 1010 |
| 3622 | 78378110 (14539, 14540) | Novel Protein sim. GBank gi 2653808 emb CAB13310 - (Z99111) similar to hypothetical proteins [Bacillus subtilis] | | UNCLASSIFIED | 1026 |
| 3623 | 37801362 (3029, 3030) | Novel Protein sim. GBank gi 2633966 emb CAB13467 - (Z99112) chromosome segregation SMC protein homolog [Bacillus subtilis] | | UNCLASSIFIED | 1012 |

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| 3624 | 20177438 (3155, 3156) | Novel Protein sim. GBank gil[2634113]emb[CAB13613] - (Z99113) multidrug resistance protein [Bacillus subtilis] | | UNCLASSIFIED | |
| 3625 | 27968845 (1929, 1930) | Novel Protein sim. GBank gil[2635246]emb[CAB14741] - (Z99118) similar to sodium/proton-dependent alanine carrier protein [Bacillus subtilis] | | UNCLASSIFIED | 1006 |
| 3626 | 91219035 (8257, 8258) | Novel Protein sim. GBank gil[2635598]emb[CAB15092] - (Z99119) similar to cysteine dioxygenase [Bacillus subtilis] | | UNCLASSIFIED | 1044 |
| 3627 | 23302606 (1417, 1418) | Novel Protein sim. GBank gil[2635736]emb[CAB15229] - (Z99120) yunF [Bacillus subtilis] | | UNCLASSIFIED | 1023 |
| 3628 | 79485383 (3293, 3294) | Novel Protein sim. GBank gil[2635857]emb[CAB15349] - (Z99121) similar to sulfite reductase [Bacillus subtilis] | | UNCLASSIFIED | 1022 |
| 3629 | 55005423 (5975, 5976) | Novel Protein sim. GBank gil[2642222 (AF030885) - telomere-associated recQ-like helicase [Ustilago maydis] | | UNCLASSIFIED | 1019 |
| 3630 | 79477093 (16119, 16120) | Novel Protein sim. GBank gil[2642222 (AF030885) - telomere-associated recQ-like helicase [Ustilago maydis] | | UNCLASSIFIED | 1038 |
| 3631 | 25149365 (10293, 10294) | Novel Protein sim. GBank gil[2645861 (AF034211) - transposase OrfB [Desulfobivirio vulgaris] | | UNCLASSIFIED | 1003 |
| 3632 | 35900228 (6663, 6664) | Novel Protein sim. GBank gil[2648185 (AE000943) - carboxylesterase (est-3) [Archaeoglobus fulgidus] | | UNCLASSIFIED | 1053 |
| 3633 | 78728870 (17517, 17518) | Novel Protein sim. GBank gil[2648509 (AE000963) - conserved hypothetical protein [Archaeoglobus fulgidus] | | UNCLASSIFIED | 1026 |
| 3634 | 20721136 (5837, 5838) | Novel Protein sim. GBank gil[2649054 (AE000998) - long-chain-fatty-acid-CoA ligase (fadD-6) [Archaeoglobus fulgidus] | | UNCLASSIFIED | 1006 |

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| 3635 | 13501107 (4547, 4548) | Novel Protein sim. GBank gi 2649711 (AE001042) - ribose ABC transporter, permease protein (rbsC-1) [Archaeoglobus fulgidus] | | |
| 3636 | 52560096 (445, 446) | Novel Protein sim. GBank gi 2650614 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus] | UNCLASSIFIED | 1003, 1034 |
| 3637 | 79581304 (14881, 14882) | Novel Protein sim. GBank gi 2655293 (AF032975) - germin-like protein 5 [Oryza sativa] | UNCLASSIFIED | 1024 |
| 3638 | 88095003 (8443, 8444) | Novel Protein sim. GBank gi 2661691 emb CAA15795 - (AL009204) putative protease [Streptomyces coelicolor] | UNCLASSIFIED | 1010, 1022 |
| 3639 | 80072425 (1363, 1364) | Novel Protein sim. GBank gi 2661697 emb CAA15801 - (AL009204) hypothetical protein SC9B10.11 [Streptomyces coelicolor] | UNCLASSIFIED | 1003, 1006, 1008, 1022, 1023, 1024, 1038 |
| 3640 | 78893730 (15593, 15594) | Novel Protein sim. GBank gi 2662167 dbj BAA23715 - (AB007903) KIAA0443 [Homo sapiens] | UNCLASSIFIED | 1000, 1003, 1008, 1017, 1026 |
| 3641 | 9945112 (4375, 4376) | Novel Protein sim. GBank gi 2662365 dbj BAA23667 - (D86332) membrane type-2 matrix metalloproteinase [Mus musculus] | UNCLASSIFIED | 1044 |
| 3642 | 94651275 (19429, 19430) | Novel Protein sim. GBank gi 266541 sp P30746 MOAB_ECOLI-MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN_B | UNCLASSIFIED | 1027 |
| 3643 | 79831223 (20635, 20636) | Novel Protein sim. GBank gi 267417 sp P29955 XANA_XANCP - PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMANNOMUTASE (PGM) / PHOSPHOMANNOMUTASE (PMM)) | UNCLASSIFIED | 1023 |
| 3644 | 19642417 (5411, 5412) | Novel Protein sim. GBank gi 2688013 (AE001124) - hemolysin III (yplQ) [Borrelia burgdorferi] | UNCLASSIFIED | 1010 |

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| 3645 | 85818145 (2245, 2246) | Novel Protein sim. GBank gi 2688536 (AE001162) - conserved hypothetical protein [Borrelia burgdorferi] | | UNCLASSIFIED | 1019 |
| 3646 | 47657227 (16139, 16140) | Novel Protein sim. GBank gi 2695636 emb CAA15906 - (AL021006) hypothetical protein Rv1250 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1026, 1029 |
| 3647 | 29647423 (13861, 13862) | Novel Protein sim. GBank gi 2695957 emb CAA15850 - (AL010186) hypothetical protein Rv1173 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1024 |
| 3648 | 10142304 (1641, 1642) | Novel Protein sim. GBank gi 2695952 emb CAA15855 - (AL010186) hypothetical protein Rv1178 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1054 |
| 3649 | 77822309 (2471, 2472) | Novel Protein sim. GBank gi 2708660 (AF037440) - putative 30.6 kDa protein [Edwardsiella ictaluri] | | UNCLASSIFIED | 1022 |
| 3650 | 32152988 (16787, 16788) | Novel Protein sim. GBank gi 2708660 (AF037440) - putative 30.6 kDa protein [Edwardsiella ictaluri] | | UNCLASSIFIED | 1023 |
| 3651 | 25266105 (2863, 2864) | Novel Protein sim. GBank gi 2708666 (AF037441) - putative 54.5 kDa protein [Edwardsiella ictaluri] | | UNCLASSIFIED | 1054 |
| 3652 | 20288333 (4147, 4148) | Novel Protein sim. GBank gi 2708666 (AF037441) - putative 54.5 kDa protein [Edwardsiella ictaluri] | | UNCLASSIFIED | 1034 |
| 3653 | 34868408 (18407, 18408) | Novel Protein sim. GBank gi 2708741 (AC003952) - hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1034 |
| 3654 | 30258500 (22937, 22938) | Novel Protein sim. GBank gi 2731767 (AF016099) - endonuclease/reverse transcriptase [Mus musculus] | | UNCLASSIFIED | 1044 |
| 3655 | 28387395 (21361, 21362) | Novel Protein sim. GBank gi 2736155 (AF022082) - sulfolipid biosynthesis protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1017 |

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| 3656 | 80025234 (12167, 12168) | Novel Protein sim. GBank gil2760909 (AF036925) - family 10 xylanase [Caldicellulosiruptor sp. R169B.1] | | UNCLASSIFIED | |
| 3657 | 27977410 (875, 876) | Novel Protein sim. GBank gil2764873[emb CAA665571] - (X97918) gene 18.1 [Bacteriophage SPP1] | | UNCLASSIFIED | 1006 |
| 3658 | 10077458 (2323, 2324) | Novel Protein sim. GBank gil2764873[emb CAA665571] - (X97918) gene 18.1 [Bacteriophage SPP1] | | UNCLASSIFIED | 1038 |
| 3659 | 27977572 (20039, 20040) | Novel Protein sim. GBank gil2764873[emb CAA665571] - (X97918) gene 18.1 [Bacteriophage SPP1] | | UNCLASSIFIED | 1006 |
| 3660 | 47652014 (18947, 18948) | Novel Protein sim. GBank gil27650811[emb CAA71589] - (Y10557) g5bf [Arabidopsis thaliana] | | UNCLASSIFIED | 1029 |
| 3661 | 11130354 (21937, 21938) | Novel Protein sim. GBank gil2765453[emb CAA75539] - (Y15252) nitrate extrusion protein [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1006 |
| 3662 | 20434582 (14167, 14168) | Novel Protein sim. GBank gil2772914 (AF029249) - procollagen D [Mytilus edulis] | | UNCLASSIFIED | 1022 |
| 3663 | 78379687 (12757, 12758) | Novel Protein sim. GBank gil2780178[emb CAA38047] - (X54111) putative enol-pyruvyltransferase [Treponema pallidum] | | UNCLASSIFIED | 1003, 1026 |
| 3664 | 20437191 (8043, 8044) | Novel Protein sim. GBank gil2791398[emb CAA15994] - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1010 |
| 3665 | 79870655 (13925, 13926) | Novel Protein sim. GBank gil2791423[emb CAA16017.1] - (AL021185) bcp [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012 |
| 3666 | 57529037 (16449, 16450) | Novel Protein sim. GBank gil2791423[emb CAA16017.1] - (AL021185) bcp [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012 |
| 3667 | 78373648 (11053, 11054) | Novel Protein sim. GBank gil2791495[emb CAA16032] - (AL021246) hypothetical protein Rv2455c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1008, 1026 |

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| 3668 | 78526486 (19473, 19474) | Novel Protein sim. GBank gi 279156 emb CAA16053] - (AL021246) hypothetical protein Rv2476c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1001, 1008, 1026, 1029 |
| 3669 | 80060189 (12139, 12140) | Novel Protein sim. GBank gi 2791626 emb CAA16113.1 - (AL021287) fixB [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1022, 1024 |
| 3670 | 38434691 (12423, 12424) | Novel Protein sim. GBank gi 2801417 (AF007777) - KpsD [Escherichia coli] | | UNCLASSIFIED | 1008 |
| 3671 | 78474846 (393, 394) | Novel Protein sim. GBank gi 280630 pir A60095 - larval glue protein Lgp-1 precursor - fruit fly (<i>Drosophila virilis</i>) | | UNCLASSIFIED | 1026 |
| 3672 | 78182342 (9261, 9262) | Novel Protein sim. GBank gi 2811055 spi O07395 YS02_MYCAV - HYPOTHETICAL 36.1 KD PROTEIN MAV335 | | UNCLASSIFIED | 1029, 1053 |
| 3673 | 10069458 (6365, 6366) | Novel Protein sim. GBank gi 2815577 (AF012101) - VceA [Vibrio cholerae] | | UNCLASSIFIED | 1012 |
| 3674 | 27923447 (3403, 3404) | Novel Protein sim. GBank gi 2822117 sp P16917 RHSB_ECOLI - RHSB PROTEIN PRECURSOR | | UNCLASSIFIED | 1004, 1010 |
| 3675 | 78700877 (12453, 12454) | Novel Protein sim. GBank gi 2826876 emb CAA76170] - (Y16311) GidB-like protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1008, 1016, 1026 |
| 3676 | 20606886 (20373, 20374) | Novel Protein sim. GBank gi 2827537 emb CAA16642] - (AL021646) hypothetical protein Rv3177 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1004 |
| 3677 | 80506698 (2239, 2240) | Novel Protein sim. GBank gi 2827539 emb CAA16644] - (AL021646) hypothetical protein Rv3179 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012, 1017, 1026 |
| 3678 | 87451432 (21977, 21978) | Novel Protein sim. GBank gi 282943 sp P52279 PIP_XANCI - PROLINE IMINOPEPTIDASE (PROLYL AMINOPEPTIDASE) | | UNCLASSIFIED | 1008, 1025 |

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| 3679 | 10082229 (4451, 4452) | Novel Protein sim. GBank gi 282952 sp P71571 YCT36_MYTCTU - HYPOTHETICAL PROTEIN CY10D7_36C | | UNCLASSIFIED | 1044 |
| 3680 | 66258664 (1917, 1918) | Novel Protein sim. GBank gi 2829802 sp P94408 YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP. GERKA INTERGENIC REGION | | UNCLASSIFIED | 1006, 1010, 1012, 1058 |
| 3681 | 78377705 (11489, 11490) | Novel Protein sim. GBank gi 2829815 sp P95095 CSTA_MYTCTU - CARBON STARVATION PROTEIN A HOMOLOG | | UNCLASSIFIED | 1026, 1029, 1053 |
| 3682 | 20477336 (20621, 20622) | Novel Protein sim. GBank gi 2829827 sp P96194 YIBL_AZ0VI - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN IBPB-LEUC INTERGENIC REGION | | UNCLASSIFIED | 1024 |
| 3683 | 29444840 (9481, 9482) | Novel Protein sim. GBank gi 2829910 (AC002291) - Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana] | | UNCLASSIFIED | 1026 |
| 3684 | 20159983 (5491, 5492) | Novel Protein sim. GBank gi 283045 pir S2B264 - hydroxyproline-rich glycoprotein - maize | | UNCLASSIFIED | 1010 |
| 3685 | 10315215 (17821, 17822) | Novel Protein sim. GBank gi 283045 pir S2B264 - hydroxyproline-rich glycoprotein - maize | | UNCLASSIFIED | 1038 |
| 3686 | 38920403 (707, 708) | Novel Protein sim. GBank gi 283264 emb CAA16719 - (AL021710) teosinte branched 1 - like protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1008 |
| 3687 | 47654615 (9877, 9878) | Novel Protein sim. GBank gi 283268 emb CAA16785_1 - (AL021712) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1029 |
| 3688 | 78519937 (15775, 15776) | Novel Protein sim. GBank gi 2833210 sp Q07729 YD3C_YEAST - HYPOTHETICAL 55.2 KD PROTEIN YDI238C | | UNCLASSIFIED | 1009 |

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| 3689 | 65709078 (12223, 12224) | Novel Protein sim. GBank gi 2833435 sp Q50004 YNTB_MYCLE - HYPOTHETICAL 41.1 KD PROTEIN (NTB) | | UNCLASSIFIED | 1023 |
| 3690 | 3580786 (5575, 5576) | Novel Protein sim. GBank gi 2833647 (AF027972) - flagelliform silk protein [Nephila clavipes] | | UNCLASSIFIED | 1012 |
| 3691 | 78761616 (18679, 18680) | Novel Protein sim. GBank gi 285118 pir S27880 - Nasopressin receptor - rat | | UNCLASSIFIED | 1017 |
| 3692 | 94686125 (18119, 18120) | Novel Protein sim. GBank gi 2851412 sp Q10817 YX27_MYCTU - HYPOTHETICAL 40.1 KD PROTEIN CY274.27C | | UNCLASSIFIED | 1001, 1054 |
| 3693 | 80245905 (1511, 1512) | Novel Protein sim. GBank gi 2851427 sp P32427 PCAB_PSEPU - 3 - CARBOXY-CIS,CIS-MUCONATE CYCLOISOMERASE (3-CARBOXYMUCONATE LACTONIZING ENZYME) (CMLE) | | UNCLASSIFIED | 1004, 1006, 1009, 1010, 1022, 1023, 1024, 1034, 1039, 1049 |
| 3694 | 10200283 (10187, 10188) | Novel Protein sim. GBank gi 2851439 sp P27351 UBIE_ECOLI - UBIQUINONE/MENAQUNONE BIOSYNTHESIS METHYLTRANSFERASE UBIE | | UNCLASSIFIED | 1039 |
| 3695 | 39362438 (7231, 7232) | Novel Protein sim. GBank gi 2851600 sp P33999 YJUG_ECOLI - HYPOTHETICAL 25.3 KD PROTEIN IN RIMI - PRFC INTERGENIC REGION | | UNCLASSIFIED | 1010, 1025 |
| 3696 | 27783323 (20295, 20296) | Novel Protein sim. GBank gi 2851600 sp P33999 YJUG_ECOLI - HYPOTHETICAL 25.3 KD PROTEIN IN RIMI - PRFC INTERGENIC REGION | | UNCLASSIFIED | 1001, 1034 |
| 3697 | 11819032 (13749, 13750) | Novel Protein sim. GBank gi 2853098 emb CAA16914 - (AL021767) vacuolar protein sorting [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1031 |

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| 3698 12554) | 20706475 (12553, Novel Protein sim. GBank gi 285355 pir B43936 - ORF 3' of ctsA - <i>Bacillus</i> sp. (fragment) | | UNCLASSIFIED | 1022 |
| 3699 6012) | 80242645 (6011, Novel Protein sim. GBank gi 2854153 (AF045640) - No definition line found [<i>Caenorhabditis elegans</i>] | | UNCLASSIFIED | 1008, 1022 |
| 3700 20686) | 13084358 (20685, Novel Protein sim. GBank gi 2854158 gb AAC02577.1 - (AF045641) No definition line found [<i>Caenorhabditis elegans</i>] | | UNCLASSIFIED | 1006, 1024 |
| 3701 8534) | 36999028 (8533, Novel Protein sim. GBank gi 2865134 dbj BA24794 - (AB001577) low specificity L-threonine aldolase [<i>Pseudomonas</i> sp.] | | UNCLASSIFIED | 1001 |
| 3702 7630) | 29353027 (7629, Novel Protein sim. GBank gi 2887409 dbj BA24847 - (AB007877) KIAA0417 [Homo sapiens] | | UNCLASSIFIED | 1008 |
| 3703 16090) | 30258387 (16089, Novel Protein sim. GBank gi 2887409 dbj BA24847 - (AB007877) KIAA0417 [Homo sapiens] | | UNCLASSIFIED | 1026 |
| 3704 14044) | 13084619 (14043, Novel Protein sim. GBank gi 2894252 emb CAA17114.1 - (AL021841) hypothetical protein Rv3342 [<i>Mycobacterium</i> tuberculosis] | | UNCLASSIFIED | 1022 |
| 3705 20754) | 79116888 (20753, Novel Protein sim. GBank gi 2896144 (AF047003) - laminarinase [<i>Rhodothermus marinus</i>] | | UNCLASSIFIED | 1013 |
| 3706 21116) | 65466539 (21115, Novel Protein sim. GBank gi 2896714 emb CAA17183.1 - (AL021897) PE_PGRS [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1010 |
| 3707 12332) | 78461255 (12331, Novel Protein sim. GBank gi 2896706 emb CAA17185.1 - (AL021897) hypothetical protein Rv1069c [<i>Mycobacterium</i> tuberculosis] | | UNCLASSIFIED | 1026 |
| 3708 16430) | 20594204 (16429, Novel Protein sim. GBank gi 2896706 emb CAA17185.1 - (AL021897) hypothetical protein Rv1069c [<i>Mycobacterium</i> tuberculosis] | | UNCLASSIFIED | 1058 |

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| 3709 | 79181031 (1031, 1032) | Novel Protein sim. GBank gij2896708 emb CAA17187.1 - (AL021897) echA9 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1027 |
| 3710 | 27341956 (9273, 9274) | Novel Protein sim. GBank gij2896715 emb CAA17194.1 - (AL021897) pra [Mycobacterium tuberculosis] | UNCLASSIFIED | 1039, 1044 |
| 3711 | 78468405 (17755, 17756) | Novel Protein sim. GBank gij2896721 emb CAA17200.1 - (AL021897) hypothetical protein Rv1084 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1026 |
| 3712 | 20457834 (16355, 16356) | Novel Protein sim. GBank gij2909464 emb CAA17350 - (AL021930) fadD27 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1010 |
| 3713 | 13084995 (753, 754) | Novel Protein sim. GBank gij2909501 emb CAA17386 - (AL021931) hypothetical protein Rv0380c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1027 |
| 3714 | 20632801 (4917, 4918) | Novel Protein sim. GBank gij2909643 emb CAA17455 - (AL021942) hypothetical protein RV0584 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1004 |
| 3715 | 28836453 (7711, 7712) | Novel Protein sim. GBank gij2911073 emb CAA17535.1 - (AL021960) putative protein [Arabidopsis thaliana] | UNCLASSIFIED | 1017 |
| 3716 | 79863543 (2821, 2822) | Novel Protein sim. GBank gij2920625 (AF044499) - vgrE protein [Escherichia coli] | UNCLASSIFIED | 1003, 1054 |
| 3717 | 14973796 (18303, 18304) | Novel Protein sim. GBank gij2920625 (AF044499) - vgrE protein [Escherichia coli] | UNCLASSIFIED | 1027 |
| 3718 | 10331526 (17165, 17166) | Novel Protein sim. GBank gij2921304 (AF033496) - herbicide safener binding protein [Zea mays] | UNCLASSIFIED | 1023 |
| 3719 | 94991905 (3385, 3386) | Novel Protein sim. GBank gij2924463 emb CAA17703 - (AL022021) hypothetical protein Rv1781c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1001, 1010, 1027, 1031, 1034, 1039 |

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| 3720 | 78677596 (9835, 9836) | Novel Protein sim. GBank gi 2924463 emb CAA17703 - (AL0222021) hypothetical protein Rv1781c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1008 |
| 3721 | 20292492 (15637, 15638) | Novel Protein sim. GBank gi 2935296 (AF037272) - WAP four-disulfide core domain protein [Rattus norvegicus] | | UNCLASSIFIED | 1022 |
| 3722 | 9896796 (2913, 2914) | Novel Protein sim. GBank gi 2947269 (AF049243) - symbiosis island integrase [Mesorhizobium loti] | | UNCLASSIFIED | 1017 |
| 3723 | 79233571 (21505, 21506) | Novel Protein sim. GBank gi 2980437 emb CAA17840 - (AL0222073) hypothetical protein Rv1967 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1001 |
| 3724 | 79572946 (15021, 15022) | Novel Protein sim. GBank gi 2950440 emb CAA17843 - (AL0222073) iprM [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1016, 1044 |
| 3725 | 42941696 (868, 870) | Novel Protein sim. GBank gi 295597 (L16548) - cell division cycle protein [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1050 |
| 3726 | 88094595 (9437, 9438) | Novel Protein sim. GBank gi 2860082 emb CAA17980.1 - (AL0222121) hypothetical protein Rv3658c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1004, 1026, 1031 |
| 3727 | 25241750 (17409, 17410) | Novel Protein sim. GBank gi 2960083 emb CAA17981.1 - (AL0222121) trbB [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1044 |
| 3728 | 9875524 (8611, 8612) | Novel Protein sim. GBank gi 2960154 emb CAA18052.1 - (AL0222121) hypothetical protein Rv3730c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1044 |
| 3729 | 79835199 (4161, 4162) | Novel Protein sim. GBank gi 2960161 emb CAA18059.1 - (AL0222121) hypothetical protein Rv3737 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1009, 1023, 1027 |

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| 3730 | 20434462 (16463) 16464) | Novel Protein sim. GBank gij296017 emb CAA18071.1 - (AL022121) hypothetical protein Rv3749c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1022 |
| 3731 | 94322180 (21317, 21318) | Novel Protein sim. GBank gij296594 emb CAA48592 - (X68600) pZE40 [Hordeum vulgare] | UNCLASSIFIED | 1044 |
| 3732 | 78925817 (8199, 8200) | Novel Protein sim. GBank gij2970646 (AF051945) - Xin [Mus musculus] | UNCLASSIFIED | 1009, 1039 |
| 3733 | 11807057 (20031, 20032) | Novel Protein sim. GBank gij2981042 (AF051650) - hydroxamate-type ferriderophore receptor [Pseudomonas aeruginosa] | UNCLASSIFIED | 1017 |
| 3734 | 99388795 (10205, 10206) | Novel Protein sim. GBank gij2981221 (AF053091) - eyelid [Drosophila melanogaster] | UNCLASSIFIED | 1003, 1004, 1010, 1012, 1017, 1044, 1054 |
| 3735 | 20747754 (14705, 14706) | Novel Protein sim. GBank gij2981221 (AF053091) - eyelid [Drosophila melanogaster] | UNCLASSIFIED | 1022 |
| 3736 | 65891394 (593, 594) | Novel Protein sim. GBank gij298163 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | UNCLASSIFIED | 1054 |
| 3737 | 86466230 (3331, 3332) | Novel Protein sim. GBank gij298163 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | UNCLASSIFIED | 1029 |
| 3738 | 32184749 (8801, 8802) | Novel Protein sim. GBank gij298163 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | UNCLASSIFIED | 1029 |
| 3739 | 70079161 (11033, 11034) | Novel Protein sim. GBank gij298163 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | UNCLASSIFIED | 1042 |
| 3740 | 90936390 (15107, 15108) | Novel Protein sim. GBank gij298163 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | UNCLASSIFIED | 1020 |
| 3741 | 94132221 (16473, 16474) | Novel Protein sim. GBank gij298163 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | UNCLASSIFIED | 1003 |

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| 1054 | Urinary System/Kidney | cancer, trauma, regeneration (in vitro and in vivo), viral/bacterial/parasitic infections | Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcemia, Lesch-Nyhan syndrome |
| 1055 | Urinary System/Kidney/Cortex | cancer, trauma, regeneration (in vitro and in vivo), viral/bacterial/parasitic infections | Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcemia, Lesch-Nyhan syndrome |
| 1056 | Urinary System/Kidney/Kidney Cortex/Nephrons/Proximal Convoluted Tubule | cancer, trauma, regeneration (in vitro and in vivo), viral/bacterial/parasitic infections | Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcemia, Lesch-Nyhan syndrome |
| 1057 | Urinary System/Urinary Bladder | cancer, trauma, regeneration (in vitro and in vivo), viral/bacterial/parasitic infections | cystitis, incontinence |
| 1058 | Whole Organism | cancer, trauma, tissue regeneration (in vitro and in vivo), viral/bacterial/parasitic infections, immunological disease, respiratory disease, gastro-intestinal diseases, reproductive health, neurological and neurodegenerative diseases, bone marrow transplantation, metabolic and endocrine diseases, allergy and inflammation, nephrological disorders, cardiovascular diseases, muscle, bone, joint and skeletal disorders, hematopoietic disorders, urinary system disorders | |

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| 3742 | 95292743 (17239, 17240) | Novel Protein sim. GBank gi 29829986 (AE000682) - putative protein [Aequifex aeolicus] | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1010, 1017, 1024, 1034, 1038, 1044 |
| 3743 | 86464818 (10959, 10960) | Novel Protein sim. GBank gi 2982990 (AE000682) - hypothetical protein [Aequifex aeolicus] | | UNCLASSIFIED | 1003, 1004, 1008, 1009, 1012, 1022, 1027, 1029, 1031, 1039 |
| 3744 | 79854963 (12121, 12122) | Novel Protein sim. GBank gi 2983155 (AE000693) - phosphoglucomutase/phosphomannomutase [Aequifex aeolicus] | | UNCLASSIFIED | 1022, 1023, 1026 |
| 3745 | 78738893 (1655, 1656) | Novel Protein sim. GBank gi 2983161 (AE000693) - hypothetical protein [Aequifex aeolicus] | | UNCLASSIFIED | 1016, 1029, 1044 |
| 3746 | 79558708 (19067, 19068) | Novel Protein sim. GBank gi 2983239 (AE000699) - penicillin binding protein 1A [Aequifex aeolicus] | | UNCLASSIFIED | 1003 |
| 3747 | 86672776 (17887, 17888) | Novel Protein sim. GBank gi 2983296 (AE000703) - N-methylhydantoinase A [Aequifex aeolicus] | | UNCLASSIFIED | 1048 |
| 3748 | 80249045 (12865, 12866) | Novel Protein sim. GBank gi 2983973 (AE000748) - hypothetical protein [Aequifex aeolicus] | | UNCLASSIFIED | 1022, 1034 |
| 3749 | 35933537 (20457, 20458) | Novel Protein sim. GBank gi 2984142 (AE000760) - proprotein translocase SecA subunit [Aequifex aeolicus] | | UNCLASSIFIED | 1053 |
| 3750 | 18568845 (9159, 9160) | Novel Protein sim. GBank gi 2984162 (AE000761) - hypothetical protein [Aequifex aeolicus] | | UNCLASSIFIED | 1001 |
| 3751 | 19847336 (891, 892) | Novel Protein sim. GBank gi 2984771 (AF054622) - PppA [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1034 |

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| 3752 | 82124653 (8679, 8680) | Novel Protein sim. GBank gi 298642 bbs 127516 - (S57132) type XVI collagen alpha 1 chain, alpha 1 (XVI) [human, placenta, Peptide Partial, 1186 aa] [Homo sapiens] | | UNCLASSIFIED | 1008, 1010, 1016, 1044, 1054 |
| 3753 | 80255581 (6159, 6160) | Novel Protein sim. GBank gi 2995273 emb CAA06222 - (AJ004922) aminopeptidase [Lycopersicon esculentum] | | UNCLASSIFIED | 1006 |
| 3754 | 11398597 (1939, 1940) | Novel Protein sim. GBank gi 2995341 emb CAA18298 - (AL022244) hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1006 |
| 3755 | 82358264 (3589, 3590) | Novel Protein sim. GBank gi 2995352 emb CAA04606.1 - (AJ001206) pep1 [Streptomyces coelicolor] | | UNCLASSIFIED | 1001, 1006, 1008, 1010, 1022, 1023, 1024, 1030, 1038 |
| 3756 | 79831387 (19009, 19010) | Novel Protein sim. GBank gi 2996039 (AF054525) - hypothetical protein [Synchococcus PCC7002] | | UNCLASSIFIED | 1023, 1039 |
| 3757 | 80059952 (21999, 22000) | Novel Protein sim. GBank gi 2996650 (AC004493) - KIAA0324 [Homo sapiens] | | UNCLASSIFIED | 1024 |
| 3758 | 85538823 (12233, 12234) | Novel Protein sim. GBank gi 3002527 (AF010144) - neuronal thread protein AD7c-NTP [Homo sapiens] | | UNCLASSIFIED | 1054 |
| 3759 | 21660522 (3583, 3584) | Novel Protein sim. GBank gi 3006178 emb CAA18398.1 - (AL022304) putative rRNA regulator [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1024 |
| 3760 | 10920989 (21697, 21698) | Novel Protein sim. GBank gi 3023676 spi P56287 E2BE_SCHPO - PROBABLE TRANSLATION INITIATION FACTOR EIF-2B EPSILON SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) | | UNCLASSIFIED | 1024 |
| 3761 | 78498961 (3341, 3342) | Novel Protein sim. GBank gi 3024154 spi Q9Z794 MOZ_HUMAN - MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN | | UNCLASSIFIED | 1016, 1024 |

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| 3762 | 80209634 (5713, 5714) | Novel Protein sim. GBank gi 3024675 sp P56471 SYY_HELPPY - TYROSYL-TRNA SYNTHETASE (TYROSINE-TRNA LIGASE) (TYRRS) | | UNCLASSIFIED | 1034 |
| 3763 | 78477090 (19523, 19524) | Novel Protein sim. GBank gi 3024715 sp O08807 TDXN_MOUSE - ANTOXIDANT ENZYME AOE372 | | UNCLASSIFIED | 1003 |
| 3764 | 3692426 (16455, 16456) | Novel Protein sim. GBank gi 3024732 sp Q58432 THIC_METJA - PROBABLE THIAMIN BIOSYNTHESIS PROTEIN THIC | | UNCLASSIFIED | 1012 |
| 3765 | 78835864 (7607, 7608) | Novel Protein sim. GBank gi 3025127 sp P76235 YEAH_ECOLI - HYPOTHETICAL 49.4 KD PROTEIN IN GAPA-RND INTERGENIC REGION | | UNCLASSIFIED | 1008 |
| 3766 | 25165226 (16229, 16230) | Novel Protein sim. GBank gi 30251621 sp P76369 YEEY_ECOLI - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SBCB-HISL INTERGENIC REGION | | UNCLASSIFIED | 1003 |
| 3767 | 79912109 (14655, 14656) | Novel Protein sim. GBank gi 3025170 sp P77500 YFER_ECOLI - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN XAPA-LIG INTERGENIC REGION | | UNCLASSIFIED | 1038 |
| 3768 | 78800814 (9037, 9038) | Novel Protein sim. GBank gi 30252761 sp Q02981 YP09_YEAST - HYPOTHETICAL 62.8 KD PROTEIN IN SSE1-CAR1 INTERGENIC REGION | | UNCLASSIFIED | 1026 |
| 3769 | 30258104 (12509, 12510) | Novel Protein sim. GBank gi 30252821 sp P77691 YR40_MYCTU - HYPOTHETICAL 35.8 KD PROTEIN CY21B4.40 | | UNCLASSIFIED | 1026 |
| 3770 | 80414655 (20159, 20160) | Novel Protein sim. GBank gi 30252841 sp P77475 YQAB_ECOLI - HYPOTHETICAL 20.8 KD PROTEIN IN GSRA-INTERGENIC REGION | | UNCLASSIFIED | 1004, 1008, 1010, 1023, 1024, 1025, 1034 |

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| 3771 | 25243584 (21071, 21072) | Novel Protein sim. GBank gij 3033380 (AC004238) - putative coatomer epsilon subunit [Arabidopsis thaliana] | | UNCLASSIFIED | 1013 |
| 3772 | 78715968 (12027, 12028) | Novel Protein sim. GBank gij 3043529[emb CAA05249] - (AJ002204) polyamine oxidase [Zea mays] | | UNCLASSIFIED | 1017 |
| 3773 | 78948406 (443, 444) | Novel Protein sim. GBank gij 3043648[dbj BAA25488] - (AB011134) KIAA0562 protein [Homo sapiens] | | UNCLASSIFIED | 1044 |
| 3774 | 38869092 (10837, 10838) | Novel Protein sim. GBank gij 3043714[dbj BAA25521] - (AB011167) KIAA0595 protein [Homo sapiens] | | UNCLASSIFIED | 1003 |
| 3775 | 56451138 (22257, 22258) | Novel Protein sim. GBank gij 3043718[dbj BAA25523] - (AB011169) KIAA0597 protein [Homo sapiens] | | UNCLASSIFIED | 1003 |
| 3776 | 23299542 (13201, 13202) | Novel Protein sim. GBank gij 3043882 (U95842) - transmembrane protein Tmp7 [Lactococcus lactis] | | UNCLASSIFIED | 1044 |
| 3777 | 78784542 (12987, 12988) | Novel Protein sim. GBank gij 3044093 (AF055999) - hypothetical protein PhuW [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1008 |
| 3778 | 79862572 (7205, 7206) | Novel Protein sim. GBank gij 3046395[gb AAC36320_1] - (AF026544) unknown [Ralstonia eutropha] | | UNCLASSIFIED | 1006, 1017 |
| 3779 | 20292854 (17149, 17150) | Novel Protein sim. GBank gij 3068553 (U19489) - Glycoprotein Ib [Canis familiaris] | | UNCLASSIFIED | 1034 |
| 3780 | 65641577 (13087, 13088) | Novel Protein sim. GBank gij 30685592 (AF026465) - punc [Mus musculus] | | UNCLASSIFIED | 1016 |
| 3781 | 79570299 (14997, 14998) | Novel Protein sim. GBank gij 3080400[emb CAA18720_1] - (AL0222603) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1017 |
| 3782 | 78676758 (21281, 21282) | Novel Protein sim. GBank gij 3080493[emb CAA18690] - (AL0222602) hypothetical protein MLCB268.24c [Mycobacterium leprae] | | UNCLASSIFIED | 1008 |

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| 3783 | 82439120 (22873) 22874) | Novel Protein sim. GBank gi 3088561 (AF059313) - myo-inositol dehydrogenase [Sinorhizobium melliloti] | | UNCLASSIFIED | 1001, 1006, 1012, 1022, 1023, 1024, 1026, 1034, 1044, 1058 |
| 3784 | 10187603 (12597, 12598) | Novel Protein sim. GBank gi 3055052 (AF010234) - ArsC [Pseudomonas aeruginosa] [Pseudomonas fluorescens] | | UNCLASSIFIED | 1003 |
| 3785 | 79485868 (9397, 9398) | Novel Protein sim. GBank gi 3087809 (L49465) - hypothetical metabolic transport protein [Pseudomonas fluorescens] | | UNCLASSIFIED | 1022 |
| 3786 | 9857702 (14403, 14404) | Novel Protein sim. GBank gi 3098342 (AF036166) - organic hydroperoxide resistance protein [Xanthomonas campestris] | | UNCLASSIFIED | 1008 |
| 3787 | 79192369 (20885, 20886) | Novel Protein sim. GBank gi 3098342 (AF036166) - organic hydroperoxide resistance protein [Xanthomonas campestris] | | UNCLASSIFIED | 1024 |
| 3788 | 80255457 (15565, 15566) | Novel Protein sim. GBank gi 3098418 (AF040944) - P140 [Mus musculus] | | UNCLASSIFIED | 1001, 1003, 1006, 1054 |
| 3789 | 20628071 (13583, 13584) | Novel Protein sim. GBank gi 309868 (L09108) - IS401 transposase subunit; putative [Pseudomonas cepacia] | | UNCLASSIFIED | 1010 |
| 3790 | 27832852 (11503, 11504) | Novel Protein sim. GBank gi 3122417 sp O33904 MURF_STRTO - PROBABLE UDP-N- ACETYLGLUCOSAMINYL-D-GLUTAMYL-L-2,6- DIAMINOPIMELATE-D-ALANYL-D-ALANYL LIGASE (UDP-MURNAc-PENTAPEPTIDE SYNTHETASE) (D-ALANYL-D-ALANINE-ADDING ENZYME) | | UNCLASSIFIED | 1022 |
| 3791 | 79572143 (20141, 20142) | Novel Protein sim. GBank gi 3122893 sp P94985 SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE-TRNA LIGASE BETA CHAIN) (PHERS) | | UNCLASSIFIED | 1008, 1023, 1029, 1039 |

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| 3792 20540) | 11605975 (20539, Novel Protein sim. GBank gi 31228931 spi P94985 SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE-TRNA LIGASE BETA CHAIN) (PHERS) | | UNCLASSIFIED | 1024 |
| 3793 17112) | 85525006 (17111, Novel Protein sim. GBank gi 31229051 spi O28687 SYM_METTH - METHIONYL-TRNA SYNTHETASE (METHIONINE-TRNA LIGASE) (METRS) | | UNCLASSIFIED | 1008, 1026, 1049 |
| 3794 1000) | 20137096 (999, Novel Protein sim. GBank gi 31229321 spi O32053 TGT_BACSU - QUEINE TRNA-RIBOSYL TRANSFERASE (TRNA- GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) | | UNCLASSIFIED | 1024 |
| 3795 6268) | 80216390 (6267, Novel Protein sim. GBank gi 31230211 spi Q96508 VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2)) | | UNCLASSIFIED | 1004, 1022 |
| 3796 20776) | 80256635 (20775, Novel Protein sim. GBank gi 31230211 spi Q96508 VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2)) | | UNCLASSIFIED | 1006 |
| 3797 10874) | 19521923 (10873, Novel Protein sim. GBank gi 31232241 spi P17731 HIS8_BACSU - HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (IMIDAZOLE ACETOL- PHOSPHATE TRANSAMINASE) | | UNCLASSIFIED | 1034 |
| 3798 (13783, 13784) | 100328610 Novel Protein sim. GBank gi 31235521 emb CAA18609 - (AL022578) dJ383P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens] | | UNCLASSIFIED | 1001, 1003, 1004, 1008, 1016, 1017, 1022, 1024, 1029, 1037, 1044, 1053, 1054 |

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| 3799 | 20459464 (4789, 4790) | Novel Protein sim. GBank gj 312736 emb CAA18902 - (AL023496) hypothetical protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1024 |
| 3800 | 39523493 (11359, 11360) | Novel Protein sim. GBank gj 3128287 (AF010496) - hypothetical protein [Rhodobacter capsulatus] | | UNCLASSIFIED | 1004 |
| 3801 | 82116318 (14233, 14234) | Novel Protein sim. GBank gj 3128302 (AF010496) - hypothetical protein [Rhodobacter capsulatus] | | UNCLASSIFIED | 1016, 1017 |
| 3802 | 79615799 (20363, 20364) | Novel Protein sim. GBank gj 3128335 (AF010496) - precorrin-3 methylase [Rhodobacter capsulatus] | | UNCLASSIFIED | 1003, 1044 |
| 3803 | 19884371 (20033, 20034) | Novel Protein sim. GBank gj 313602 emb CAA19102 - (AL023591) hypothetical protein MLCB1259.27 [Mycobacterium leprae] | | UNCLASSIFIED | 1034 |
| 3804 | 17936961 (9697, 9698) | Novel Protein sim. GBank gj 313605 emb CAA19115 - (AL023592) RanBP7/importin-beta1/Cse1p superfamily protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1008 |
| 3805 | 28462243 (6735, 6736) | Novel Protein sim. GBank gj 3142291 (AC002411) gb AF012921 from Magnaporthe grisea. EST gb Z224512 comes from this gene. [Arabidopsis thaliana] | | UNCLASSIFIED | 1030 |
| 3806 | 78675175 (12547, 12548) | Novel Protein sim. GBank gj 3142297 (AC002411) - Contains similarity to serine/threonine protein phosphatase gb X83099 from <i>S. cerevisiae</i> . [Arabidopsis thaliana] | | UNCLASSIFIED | 1017 |
| 3807 | 28992682 (14877, 14878) | Novel Protein sim. GBank gj 3150479 (AF067212) - partial CDS [Caenorhabditis elegans] | | UNCLASSIFIED | 1044 |
| 3808 | 16510691 (17581, 17582) | Novel Protein sim. GBank gj 3169045 emb CAA19243 - (AL023702) uroporphyrinogen decarboxylase [Streptomyces coelicolor] | | UNCLASSIFIED | 1044 |

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|------|-------------------------|---|--|--------------|------------------|
| 3809 | 79229835 (18565, 18566) | Novel Protein sim. GBank gil3169045 emb[CAA19243] - (AL023702) uroporphyrinogen decarboxylase [Streptomyces coelicolor] | | UNCLASSIFIED | 1023 |
| 3810 | 56499770 (8791, 8792) | Novel Protein sim. GBank gil3170176 gb [AAC18037.1] - (AF039688) antigen NY-GO-3 [Homo sapiens] | | UNCLASSIFIED | 1023, 1038, 1039 |
| 3811 | 80447820 (5239, 5240) | Novel Protein sim. GBank gil3171904 emb[CAA75869] - (Y15908) DIA-12C protein [Homo sapiens] | | UNCLASSIFIED | 1024 |
| 3812 | 13519669 (20053, 20054) | Novel Protein sim. GBank gil3183185 spi O076311TYP_A_BACSU - GTP-BINDING PROTEIN TYP_A/BIP_A HOMOLOG | | UNCLASSIFIED | 1022 |
| 3813 | 79443070 (22617, 22618) | Novel Protein sim. GBank gil3183185 spi O076311TYP_A_BACSU - GTP-BINDING PROTEIN TYP_A/BIP_A HOMOLOG | | UNCLASSIFIED | 1017 |
| 3814 | 26328062 (21129, 21130) | Novel Protein sim. GBank gil3183467 spi O317271YLME_BACSU - HYPOTHETICAL 25.7 KD PROTEIN IN SIGG-DIVIVA INTERGENIC REGION | | UNCLASSIFIED | 1017 |
| 3815 | 65902617 (9011, 9012) | Novel Protein sim. GBank gil3192889 (AF068843) - dihydroxy-acid dehydratase [Streptomyces coelicolor] | | UNCLASSIFIED | 1023 |
| 3816 | 58223763 (5393, 5394) | Novel Protein sim. GBank gil320748 pir [S25330 - probable membrane protein YBL011w - yeast (Saccharomyces cerevisiae)] | | UNCLASSIFIED | 1006, 1022 |
| 3817 | 39371622 (17687, 17688) | Novel Protein sim. GBank gil3218410 emb[CAA19574.1] - (AL023859) SPBC19C7.06, putative prolyl-tRNA synthetase, len:71 6aa, similar eg. to YHR020W, YH10_YEAST_P38708, putative prolyl-tRNA synthetase yhr02, (688aa), fasta scores, opt2486, E():0, (55.1% identity in 682 aa over... | | UNCLASSIFIED | 1024, 1034 |

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|------|----------------------------|--|--|--------------|------------------|
| 3818 | 67452021 (18849) 18850) | Novel Protein sim. GBank gi 3236247 (AC004684) - SCARECROW-like protein [Arabidopsis thaliana] | | | |
| 3819 | 85817932 (861, 862) | Novel Protein sim. GBank gi 3236351 (AF033863) - PRP4 protein kinase homolog [Mus musculus] | | UNCLASSIFIED | 1019 |
| 3820 | 36991783 (22215, 22216) | Novel Protein sim. GBank gi 321969 (U79580) - CtpA [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1016 |
| 3821 | 80503426 (18827, 18828) | Novel Protein sim. GBank gi 3242273 emb CAB070171 - (Z92669) hypothetical protein Rv0236c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012 |
| 3822 | 32434178 (16725, 16726) | Novel Protein sim. GBank gi 3242281 emb CAA166691 - (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012 |
| 3823 | 46665821 (1425, 1426) | Novel Protein sim. GBank gi 3252868 (AF033536) - putative zinc transporter [Arabidopsis thaliana] | | UNCLASSIFIED | 1031, 1050, 1054 |
| 3824 | 79319731 (4099, 4100) | Novel Protein sim. GBank gi 3253197 (AF029714) - PhAA [Pseudomonas putida] | | UNCLASSIFIED | 1053 |
| 3825 | 19860967 (3961, 3962) | Novel Protein sim. GBank gi 3256806 dbj BAA29289_1 - (AP000001) 171aa long hypothetical protein [Pyrococcus horikoshii] | | UNCLASSIFIED | 1001 |
| 3826 | 80027689 (19839, 19840) | Novel Protein sim. GBank gi 32566921 dbj BAA29375_1 - (AP000001) 380aa long hypothetical Na(+)/H(+) antiporter [Pyrococcus horikoshii] | | UNCLASSIFIED | 1004, 1024 |
| 3827 | 79568056 (18877, 18878) | Novel Protein sim. GBank gi 3256835 dbj BAA29518 - (AP000002) 393aa long hypothetical protein [Pyrococcus horikoshii] | | UNCLASSIFIED | 1044 |
| 3828 | 11088295 (15335, 15336) | Novel Protein sim. GBank gi 3257161 dbj BAA29844 - (AP000003) 464aa long hypothetical protein [Pyrococcus horikoshii] | | UNCLASSIFIED | 1004 |

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| 3829 | 47652238 (1043, 1044) | Novel Protein sim. GBank gi 3261660 emb CAB03752 - (Z81368) hypothetical protein Rv2420c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1029, 1034, 1053 |
| 3830 | 78891013 (6169, 6170) | Novel Protein sim. GBank gi 3261661 emb CAB03753 - (Z81368) hypothetical protein Rv2421c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1003, 1039 |
| 3831 | 95005747 (2237, 2238) | Novel Protein sim. GBank gi 3261740 emb CAB08320 - (Z95120) lpV (Mycobacterium tuberculosis) | | UNCLASSIFIED | 1034 |
| 3832 | 80467071 (12663, 12664) | Novel Protein sim. GBank gi 3261775 emb CAB09037 - (Z95584) hypothetical protein Rv1165 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012, 1039 |
| 3833 | 36827011 (22975, 22976) | Novel Protein sim. GBank gi 3261775 emb CAB09037 - (Z95584) hypothetical protein Rv1165 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1054 |
| 3834 | 39517741 (4851, 4852) | Novel Protein sim. GBank gi 3261773 emb CAB08931 - (Z95556) hypothetical protein Rv2511 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1004, 1006, 1010, 1024 |
| 3835 | 79319279 (9857, 9858) | Novel Protein sim. GBank gi 3283977 (AF072816) - ABC-type transporter MRP3 [Rattus norvegicus] | | UNCLASSIFIED | 1006, 1017, 1034 |
| 3836 | 91012911 (14087, 14088) | Novel Protein sim. GBank gi 32879511 sp O34617 YILON_BACSU - HYPOTHETICAL 41.6 KD PROTEIN IN FMT- SPOVM INTERGENIC REGION | | UNCLASSIFIED | 1010 |
| 3837 | 79846075 (7491, 7492) | Novel Protein sim. GBank gi 3288157 emb CAA11510 - (AJ223631) hypothetical protein [Escherichia coli] | | UNCLASSIFIED | 1034 |
| 3838 | 37019662 (10921, 10922) | Novel Protein sim. GBank gi 3294236 emb CAA19849 - (AL031031) putative sensory histidine kinase [Streptomyces coelicolor] | | UNCLASSIFIED | 1025 |

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| 3839 11422) | 34394203 (11421, Novel Protein sim. GBank gi 3294238 emb CAA19851 - (AL031031) ftsK homolog [Streptomyces coelicolor] | | UNCLASSIFIED | 1026 |
| 3840 80248954 (3613, 3614) | Novel Protein sim. GBank gi 3294242 emb CAA19855 - (AL031031) hypothetical protein SC7C7.09 [Streptomyces coelicolor] | | UNCLASSIFIED | 1001, 1006, 1034 |
| 3841 79846720 (3625, 3626) | Novel Protein sim. GBank gi 329782 emb CAA19879.1 - (AL031032) extensin-like protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1003, 1023, 1044 |
| 3842 25140253 (22427, 22428) | Novel Protein sim. GBank gi 329782 emb CAA19879.1 - (AL031032) extensin-like protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1003, 1022 |
| 3843 11705900 (7683, 7684) | Novel Protein sim. GBank gi 3318897 pdb 1FOH A - Chain A, Phenol Hydroxylase From Trichosporon Cutaneum | | UNCLASSIFIED | 1022 |
| 3844 37798103 (5127, 5128) | Novel Protein sim. GBank gi 3319337 (AF076530) - cell division protein FtsZ [Synechococcus PCC7942] | | UNCLASSIFIED | 1012 |
| 3845 21056486 (3599, 3600) | Novel Protein sim. GBank gi 3319741 emb CAA19907 - (AL031035) hypothetical protein SC6A9.22c [Streptomyces coelicolor] | | UNCLASSIFIED | 1004, 1022 |
| 3846 78385459 (6633, 6634) | Novel Protein sim. GBank gi 3319741 emb CAA19907 - (AL031035) hypothetical protein SC6A9.22c [Streptomyces coelicolor] | | UNCLASSIFIED | 1023, 1026 |
| 3847 10330018 (17617, 17618) | Novel Protein sim. GBank gi 3522862 (AE001232) - Tp70 protein [Treponema pallidum] | | UNCLASSIFIED | 1038 |
| 3848 79624944 (10457, 10458) | Novel Protein sim. GBank gi 3522940 (AE001239) - histidyl-tRNA synthetase (hisS) [Treponema pallidum] | | UNCLASSIFIED | 1006 |
| 3849 36625389 (21381, 21382) | Novel Protein sim. GBank gi 3327216 dbj BAA31676 - (AB014601) KIAA0701 protein [Homo sapiens] | | UNCLASSIFIED | 1034 |

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| 3850 | 11759414 (14311, 14312) | Novel Protein sim. GBank gi 3327262 dbj BAA3695 - (AB010827) NhaP [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1024 |
| 3851 | 29350796 (12751, 12752) | Novel Protein sim. GBank gi 3328717 (AE001302) - Valyl tRNA Synthetase [Chlamydia trachomatis] | | UNCLASSIFIED | 1017, 1022 |
| 3852 | 78675172 (12297, 12298) | Novel Protein sim. GBank gi 3329429 (AF049613) - huntingtin interacting protein HYPK [Homo sapiens] | | UNCLASSIFIED | 1009 |
| 3853 | 79749080 (8275, 8276) | Novel Protein sim. GBank gi 3334173 sp O05834 ERA_MYCTU - GTP- BINDING PROTEIN ERA_HOMOLOG | | UNCLASSIFIED | 1004, 1017, 1023 |
| 3854 | 78728420 (3575, 3576) | Novel Protein sim. GBank gi 3334982 (AC005306) - R27216_1 [Homo sapiens] | | UNCLASSIFIED | 1022 |
| 3855 | 78778238 (7581, 7582) | Novel Protein sim. GBank gi 3335366 (AC003028) - unknown protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1044 |
| 3856 | 6313219 (20937, 20938) | Novel Protein sim. GBank gi 3341678 emb CAA13133 - (AJ231091) z29f [Vibrio cholerae] | | UNCLASSIFIED | 1058 |
| 3857 | 79847568 (12649, 12650) | Novel Protein sim. GBank gi 3341660 emb CAA13164 - (AJ231122) z61f [Vibrio cholerae] | | UNCLASSIFIED | 1023, 1039 |
| 3858 | 78527927 (9345, 9346) | Novel Protein sim. GBank gi 3355671 emb CAA19971 - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor] | | UNCLASSIFIED | 1030 |
| 3859 | 79779458 (20763, 20764) | Novel Protein sim. GBank gi 3355671 emb CAA19971 - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor] | | UNCLASSIFIED | 1010, 1017, 1022, 1023, 1034, 1044 |
| 3860 | 81820351 (16747, 16748) | Novel Protein sim. GBank gi 3355678 emb CAA19978 - (AL031124) putative secreted protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1053, 1054 |

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| 3861 | 80017304 (11931, 11932) | Novel Protein sim. GBank gi 3367751emb CAA20089 - (AL031155) putative transcriptional regulator [Streptomyces coelicolor] | | UNCLASSIFIED | 1017, 1022, 1024 |
| 3862 | 10368042 (18103, 18104) | Novel Protein sim. GBank gi 3378352 AF079317 - DNA helicase [Sphingomonas aromaticivorans] | | UNCLASSIFIED | 1001 |
| 3863 | 95001909 (8211, 8212) | Novel Protein sim. GBank gi 3399676 AC005390 - R31180_1 [Homo sapiens] | | UNCLASSIFIED | 1004, 1010, 1034 |
| 3864 | 29213147 (17723, 17724) | Novel Protein sim. GBank gi 3402247emb CAA20183 - (AL031184) oligopeptide ABC transporter ATP-binding protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1026 |
| 3865 | 25254288 (19705, 19706) | Novel Protein sim. GBank gi 34022551emb CAA20191 - (AL031184) tRNA (5'- methylaminomethyl-2'-thiouridylate)- methyltransferase [Streptomyces coelicolor] | | UNCLASSIFIED | 1008 |
| 3866 | 65902132 (4697, 4698) | Novel Protein sim. GBank gi 3406759 AF079502 - CAMP factor [Streptococcus pyogenes] | | UNCLASSIFIED | 1023, 1044 |
| 3867 | 85801868 (12025, 12026) | Novel Protein sim. GBank gi 3406759 AF079502 - CAMP factor [Streptococcus pyogenes] | | UNCLASSIFIED | 1038, 1040 |
| 3868 | 80255569 (3057, 3058) | Novel Protein sim. GBank gi 3411177 AF076240 - Mocc [Rhizobium leguminosarum bv. viciae] | | UNCLASSIFIED | 1006, 1026 |
| 3869 | 78271019 (5289, 5290) | Novel Protein sim. GBank gi 3413391emb CAA20252 - (AL031231) hypothetical protein SC3C3.03c [Streptomyces coelicolor] | | UNCLASSIFIED | 1029 |
| 3870 | 33205346 (1025, 1026) | Novel Protein sim. GBank gi 3413411emb CAA20272 - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidylyltransferase [Streptomyces coelicolor] | | UNCLASSIFIED | 1026 |

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| 3871 | 80494518 (18289, 18290) | Novel Protein sim. GBank gi 3413628 emb CAA20296 - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor] | | UNCLASSIFIED | 1001, 1003, 1012, 1024 |
| 3872 | 56152202 (22843, 22844) | Novel Protein sim. GBank gi 3420233 (AF058763) - uroporphyrinogen decarboxylase [Zea mays] | | UNCLASSIFIED | 1008 |
| 3873 | 91215789 (9645, 9646) | Novel Protein sim. GBank gi 3420605 gb AAC31904.1 - (AF075709) putative sulfonate binding protein precursor [Pseudomonas putida] | | UNCLASSIFIED | 1016 |
| 3874 | 24135051 (13909, 13910) | Novel Protein sim. GBank gi 3420605 gb AAC31904.1 - (AF075709) putative sulfonate binding protein precursor [Pseudomonas putida] | | UNCLASSIFIED | 1003 |
| 3875 | 70947186 (16505, 16506) | Novel Protein sim. GBank gi 3426176 dbj BAA32403 - (AB008771) beta-N- Acetylglucosaminidase [Streptomyces thermophilaceus] | | UNCLASSIFIED | 1029 |
| 3876 | 56333142 (12839, 12840) | Novel Protein sim. GBank gi 3449110 emb CAA20016 - (AL031130) 1- evidence=predicted by content; 1- method=genefinder; 084; 1-method_score=257.34; 1-evidence_end; 2-evidence=predicted by motif; 2- match_accession=PROSITE:PS00343; 2- match_description=Gram-positive coccii surface proto... | | UNCLASSIFIED | 1046 |
| 3877 | 13070340 (21591, 21592) | Novel Protein sim. GBank gi 3449249 emb CAA20393 - (AL031317) putative integral membrane protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1024 |
| 3878 | 54994566 (11757, 11758) | Novel Protein sim. GBank gi 3449267 emb CAA20411 - (AL031317) putative transcriptional regulator [Streptomyces coelicolor] | | UNCLASSIFIED | 1029 |

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| 3879 | 80071696 (8863, 8864) | Novel Protein sim. GBank gi 3449270 emb CAA20414 - (AL031317) hypothetical protein SC6G4.36c [Streptomyces coelicolor] | | UNCLASSIFIED | 1022, 1023, 1031, 1034, 1039, 1053 |
| 3880 | 563333082 (2857, 2858) | Novel Protein sim. GBank gi 3449294 dbj BAA32462 - (AB011532) MEGF6 [Rattus norvegicus] | | UNCLASSIFIED | 1046 |
| 3881 | 80194752 (3119, 3120) | Novel Protein sim. GBank gi 3451473 emb CAA20490.1 - (AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1003, 1004, 1006, 1008, 1022, 1034 |
| 3882 | 36625429 (1073, 1074) | Novel Protein sim. GBank gi 345752 pir S20028 - aspartate transaminase (EC 2.6.1.1) (clone 8C7) - human | | UNCLASSIFIED | 1034 |
| 3883 | 18598551 (18809, 18810) | Novel Protein sim. GBank gi 346712 pir JC7456 - gelatinase B (EC 3.4.24.35) precursor - mouse | | UNCLASSIFIED | 1023 |
| 3884 | 80221530 (16527, 16528) | Novel Protein sim. GBank gi 347493 (L22072) - PET112 protein [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1003, 1022, 1023, 1024, 1025, 1027, 1038 |
| 3885 | 16387342 (4429, 4430) | Novel Protein sim. GBank gi 3482880 (U63816) - unknown protein [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1003 |
| 3886 | 11696124 (20807, 20808) | Novel Protein sim. GBank gi 3482881 (U63816) - unknown [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1034 |
| 3887 | 13526199 (14681, 14682) | Novel Protein sim. GBank gi 348415 pir S29383 - hisH protein - Zymomonas mobilis | | UNCLASSIFIED | 1027 |
| 3888 | 95010016 (17211, 17212) | Novel Protein sim. GBank gi 3493654 (AF093219) - transcription activator [Azospirillum brasilense] | | UNCLASSIFIED | 1044 |
| 3889 | 7523998 (1643, 1644) | Novel Protein sim. GBank gi 3510505 (AF030881) - pol polyprotein [Fugu rubripes] | | UNCLASSIFIED | 1058 |
| 3890 | 79820994 (7385, 7386) | Novel Protein sim. GBank gi 3510629 (AF047828) - syringomycin synthetase [Pseudomonas syringae pv. syringae] | | UNCLASSIFIED | 1039 |

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| 3891 | 65480226 (5421, 5422) | Novel Protein sim. GBank gil3550582 emb CAA066650 - (AJ005645) sdrc [Staphylococcus aureus] | | UNCLASSIFIED | 1054 |
| 3892 | 78896598 (21241, 21242) | Novel Protein sim. GBank gil3550954 (J64030) - dUTPase [Rattus norvegicus] | | UNCLASSIFIED | 1008, 1016, 1038, 1039 |
| 3893 | 79604379 (12703, 12704) | Novel Protein sim. GBank gil3551791 (AF047823) - cyclic beta 1-2 glucan synthetase [Brucella abortus] | | UNCLASSIFIED | 1034 |
| 3894 | 79555424 (7167, 7168) | Novel Protein sim. GBank gil3559993 emb CAA20615 - (AL031515) putative transcriptional regulator [Streptomyces coelicolor] | | UNCLASSIFIED | 1038 |
| 3895 | 80098550 (7677, 7678) | Novel Protein sim. GBank gil3599940 (AF07368) - faciogenital dysplasia protein 2 [Mus musculus] | | UNCLASSIFIED | 1022, 1025 |
| 3896 | 27846167 (1811, 1812) | Novel Protein sim. GBank gil3638957 (AC004877) - sco-spondin-mucin-like; similar to P98167 (PID:g171548); details of intron/exon structure uncertain [Homo sapiens] | | UNCLASSIFIED | 1022, 1034 |
| 3897 | 85809924 (3047, 3048) | Novel Protein sim. GBank gil3641340 gb AAC36351 - (AF090329) cyclohexanone monooxygenase homolog [Pseudomonas fluorescens] | | UNCLASSIFIED | 1038 |
| 3898 | 27837618 (9453, 9454) | Novel Protein sim. GBank gil3641337 emb CAA18824,1 - (AL023094) Nonclathrin coat protein gamma-like protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1010, 1022 |
| 3899 | 27807038 (9939, 9940) | Novel Protein sim. GBank gil3649748 emb CAA09618 - (AJ011416) IgG Fc binding protein [Mus musculus] | | UNCLASSIFIED | 1004, 1024 |
| 3900 | 17260914 (15273, 15274) | Novel Protein sim. GBank gil3660469 emb CAA05024 - (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] | | UNCLASSIFIED | 1039 |
| 3901 | 39517841 (21683, 21684) | Novel Protein sim. GBank gil3676693 (AF083949) - DNA polymerase; DnaE [Treponema denticola] | | UNCLASSIFIED | 1006 |

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| 3902 | 9217916 (21699, 21700) | Novel Protein sim. GBank gil 3688350 emb CAA19741.1 - (AL030996) dJ1189B24.4 (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8) [Homo sapiens] | | UNCLASSIFIED | 1022 |
| 3903 | 36732739 (3837, 3838) | Novel Protein sim. GBank gil 3695025 (AF056031) - Kynurenine 3-hydroxylase [Rattus norvegicus] | | UNCLASSIFIED | 1008, 1026 |
| 3904 | 20732929 (1895, 1896) | Novel Protein sim. GBank gil 3721912 dbj BAA33743.1 - (AB017156) gob-5 [<i>Mus musculus</i>] | | UNCLASSIFIED | 1024 |
| 3905 | 20720703 (8101, 8102) | Novel Protein sim. GBank gil 3724326 dbj BAA33615.1 - (AB012956) unknown [<i>Vibrio cholerae</i>] | | UNCLASSIFIED | 1006 |
| 3906 | 78989267 (14333, 14334) | Novel Protein sim. GBank gil 3732 emb CAA306931 - (X07846) GCD1 gene product (AA 1 - 511) [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1017, 1039 |
| 3907 | 11076524 (10745, 10746) | Novel Protein sim. GBank gil 3746666 (AF076848) - trihydroxytoluene oxygenase [Burkholderia cepacia] | | UNCLASSIFIED | 1010 |
| 3908 | 17930361 (9667, 9668) | Novel Protein sim. GBank gil 3747107 (AF095741) - unknown [Rattus norvegicus] | | UNCLASSIFIED | 1023 |
| 3909 | 80027758 (13771, 13772) | Novel Protein sim. GBank gil 375756 emb CAA21315 - (AL031863) 1- evidence-predicted by content; 1-method=genefinder; 084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster] | | UNCLASSIFIED | 1006, 1029 |
| 3910 | 79751800 (18095, 18096) | Novel Protein sim. GBank gil 3766365 emb CAA21417 - (AL031907) putative cystine-rich transcriptional regulator [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1004 |
| 3911 | 78759865 (12875, 12876) | Novel Protein sim. GBank gil 3777596 (AF095791) - TACC2 protein [Homo sapiens] | | UNCLASSIFIED | 1008, 1022 |

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| 3912 | 20459875 (18239, 18240) | Novel Protein sim. GBank gi 3786001 (AC005499) - unknown protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1024 |
| 3913 | 25236760 (9091, 9092) | Novel Protein sim. GBank gi 38000830 gb AAC688885 - (AF078779) putative four repeat ion channel [Rattus norvegicus] | | UNCLASSIFIED | 1003 |
| 3914 | 28308249 (19957, 19958) | Novel Protein sim. GBank gi 3808292 (AF072440) - GTPase [Enterobacter gergoviae] | s | UNCLASSIFIED | 1003 |
| 3915 | 36996223 (8657, 8658) | Novel Protein sim. GBank gi 3810873 dbj BAA34062 - (AB010465) lactonohydrolase [Fusarium oxysporum] | | UNCLASSIFIED | 1001 |
| 3916 | 9723920 (5019, 5020) | Novel Protein sim. GBank gi 3820484 (AF034373) - ataxin-2-like protein A2LP [Homo sapiens] | | UNCLASSIFIED | 1038, 1039 |
| 3917 | 24109075 (1663, 1664) | Novel Protein sim. GBank gi 3822036 (AF072326) - endo-1,3-1,4-beta-D-glucanase [Zea mays] | | UNCLASSIFIED | 1053 |
| 3918 | 19858634 (4073, 4074) | Novel Protein sim. GBank gi 3850084 emb CAA21911.1 - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1034 |
| 3919 | 34394260 (19085, 19086) | Novel Protein sim. GBank gi 3850152 emb CAA21952 - (AL033396) hypothetical protein [Candida albicans] | | UNCLASSIFIED | 1026 |
| 3920 | 13089085 (16051, 16052) | Novel Protein sim. GBank gi 3851545 gb AAC72350 - (AF079234) MreB [Vibrio cholerae] | | UNCLASSIFIED | 1027 |
| 3921 | 78519203 (21779, 21780) | Novel Protein sim. GBank gi 3851632 (AF097723) - hematopoietic lineage switch 2 related protein [Rattus norvegicus] | | UNCLASSIFIED | 1003 |
| 3922 | 78468067 (3555, 3556) | Novel Protein sim. GBank gi 38860635 emb CAA14536 - (AJ235270) ARGINYL-TRNA SYNTHETASE (args) [Rickettsia prowazekii] | | UNCLASSIFIED | 1039 |

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| 3923 | 10053411 (20627, 20628) | Novel Protein sim. GBank gi 3860646 emb CAA14547 - (AJ235270) unknown [Rickettsia prowazekii] | | UNCLASSIFIED | 1017 |
| 3924 | 17940086 (873, 874) | Novel Protein sim. GBank gi 3860724 emb CAA14625 - (AJ235270) MULTIDRUG RESISTANCE PROTEIN B (emrB) [Rickettsia prowazekii] | | UNCLASSIFIED | 1039 |
| 3925 | 77520608 (21341, 21342) | Novel Protein sim. GBank gi 3860930 emb CAA14830 - (AJ235271) tRNA SYNTHETASE (lysS) [Rickettsia prowazekii] | | UNCLASSIFIED | 1023, 1049 |
| 3926 | 9845477 (15603, 15604) | Novel Protein sim. GBank gi 3861106 emb CAA15006 - (AJ235272) unknown [Rickettsia prowazekii] | | UNCLASSIFIED | 1023 |
| 3927 | 24114042 (9291, 9292) | Novel Protein sim. GBank gi 3861107 emb CAA15007 - (AJ235272) unknown [Rickettsia prowazekii] | | UNCLASSIFIED | 1044 |
| 3928 | 13041883 (8661, 8662) | Novel Protein sim. GBank gi 3861336 emb CAA15235 - (AJ235273) unknown [Rickettsia prowazekii] | | UNCLASSIFIED | 1024 |
| 3929 | 66556191 (9465, 9466) | Novel Protein sim. GBank gi 3861430 emb CAA22035 - (ALD33505) hypothetical protein SC1E6.07 [Streptomyces coelicolor] | | UNCLASSIFIED | 1023 |
| 3930 | 80048280 (18469, 18470) | Novel Protein sim. GBank gi 3861444 emb CAA22049 - (AL033505) ABC transporter ATP-binding protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1004, 1034, 1039 |
| 3931 | 20212376 (14801, 14802) | Novel Protein sim. GBank gi 3868935 dbj BAA34293 - (AB015023) MurC [Corynebacterium glutamicum] | | UNCLASSIFIED | 1010 |
| 3932 | 20727907 (5881, 5882) | Novel Protein sim. GBank gi 3868940 dbj BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus] | | UNCLASSIFIED | 1006 |

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| 3933 | 9868440 (3663, 3664) | Novel Protein sim. GBank gil3873550 emb CAA22127 - (AL033534) serine-rich protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1008 |
| 3934 | 23333239 (4121, 4122) | Novel Protein sim. GBank gil3873550 emb CAA22127 - (AL033534) serine-rich protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1053 |
| 3935 | 79585543 (6257, 6258) | Novel Protein sim. GBank gil3875537 emb CAA91320.1 - (Z66511) similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST CEMSAD01F comes from this gene; cDNA EST CEMSAD01R comes from this gene; cDNA EST EMBL:T01268 comes from this gene; cDNA EST EMBL:D37044 comes f... | | UNCLASSIFIED | 1054 |
| 3936 | 23299986 (6807, 6808) | Novel Protein sim. GBank gil3875521 emb CAB04059 - (Z81495) predicted using Genefinder [Caenorhabditis elegans] | | UNCLASSIFIED | 1044 |
| 3937 | 94146710 (17179, 17180) | Novel Protein sim. GBank gil3875726 emb CAA91030 - (Z54270) similar to nir like gene involved in denitrification; cDNA EST EMBL:D27430 comes from this gene; cDNA EST EMBL:D27432 comes from this gene; cDNA EST EMBL:D27431 comes from this gene; cDNA EST EMBL:D33667 comes from thi... | | UNCLASSIFIED | 1003 |
| 3938 | 55474436 (4305, 4306) | Novel Protein sim. GBank gil3877422 emb CAB05195.1 - (Z82268) predicted using Genefinder; similar to CUTICLE COLLAGEN 34; cDNA EST EMBL:D65629 comes from this gene; cDNA EST EMBL:D68754 comes from this gene; cDNA EST EMBL:D68791 comes from this gene; cDNA EST EMBL:D68988 comes ... | | UNCLASSIFIED | 1026 |

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| 3939 | 79574576 (2611, 2512) | Novel Protein sim. GBank gj 3877738 emb CAAA98949 - (Z74473) predicted using Genefinder [Caenorhabditis elegans] | | | |
| 3940 | 27361342 (8423, 6424) | Novel Protein sim. GBank gj 3881524 emb CAA93883 - (Z70038) ZK1067.4 [Caenorhabditis elegans] | | UNCLASSIFIED | 1023 |
| 3941 | 87454308 (21791, 21792) | Novel Protein sim. GBank gj 3881976 emb CAA10008 - (AJ012409) hypothetical protein [Homo sapiens] | | UNCLASSIFIED | 1025 |
| 3942 | 6649815 (5441, 5442) | Novel Protein sim. GBank gj 3882185 dbj BAA34452.1 - (AB018275) KIAA0732_protein [Homo sapiens] | | UNCLASSIFIED | 1029 |
| 3943 | 8502066 (21961, 21962) | Novel Protein sim. GBank gj 3885988 (AF103809) - Ap-3 complex beta3A subunit [Mus musculus] | | UNCLASSIFIED | 1024 |
| 3944 | 5472309 (18139, 18140) | Novel Protein sim. GBank gj 38894172 (AC005312) - putative cinnamoyl-CoA reductase [Arabidopsis thaliana] | | UNCLASSIFIED | 1058 |
| 3945 | 20697087 (6089, 6090) | Novel Protein sim. GBank gj 3901272 (AF067656) - ZW10 interactor Zwint [Homo sapiens] | | UNCLASSIFIED | 1034, 1058 |
| 3946 | 30506233 (13837, 13838) | Novel Protein sim. GBank gj 3901272 (AF067656) - ZW10 interactor Zwint [Homo sapiens] | | UNCLASSIFIED | 1009 |
| 3947 | 95292917 (20971, 20972) | Novel Protein sim. GBank gj 3913029 sp P94967 ALR_MYCSM - ALANINE RACEMASE | | UNCLASSIFIED | 1010, 1024, 1034 |
| 3948 | 80502395 (22699, 22700) | Novel Protein sim. GBank gj 3913089 sp P94992 ARGR_MYCTU - PROBABLE ARGinine REPRESSOR | | UNCLASSIFIED | 1012 |
| 3949 | 79763719 (19661, 19662) | Novel Protein sim. GBank gj 3913102 sp O50175 ASTB_PSEAE - SUCCINYLARGININE DIHYDROLASE | | UNCLASSIFIED | 1008 |
| 3950 | 11089897 (22549, 22550) | Novel Protein sim. GBank gj 3913855 sp Q69162 ERA_BRAJA - GTP-BINDING PROTEIN ERA HOMOLOG | | UNCLASSIFIED | 1006 |

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| 3951 | 79830615 (16681, 16682) | Novel Protein sim. GBank gi 3914254 sp O06875 P39_BRUAB - IMMUNOGENIC 39 KD PROTEIN | | UNCLASSIFIED | 1039 |
| 3952 | 87112829 (1471, 1472) | Novel Protein sim. GBank gi 3914489 sp O32333 PTHB_CLOBE - PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIBC COMPONENT (EIIBC-GUT) (GLUCITOL/SORBITOL-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II BC COMPONENT) (EI-GUT) | | UNCLASSIFIED | 1008, 1018, 1026 |
| 3953 | 10103453 (14839, 14840) | Novel Protein sim. GBank gi 3915143 sp O31741 TRMD_BACSU - tRNA (GUANINE-N1)-METHYLTRANSFERASE (M1G-METHYLTRANSFERASE) (tRNA [GM37] METHYLTRANSFERASE) | | UNCLASSIFIED | 1012 |
| 3954 | 11776548 (10509, 10510) | Novel Protein sim. GBank gi 3914407 sp O58584 YA28_FYRHO - HYPG21HETICAL PROTEIN_PHA1028 | | UNCLASSIFIED | 1022 |
| 3955 | 79487814 (4843, 4844) | Novel Protein sim. GBank gi 3915450 sp P76270 YEBCR_ECOLI - HYPOTHETICAL 20.3 KD PROTEIN IN PRC-PPHA INTERGENIC REGION | | UNCLASSIFIED | 1006 |
| 3956 | 80027421 (18883, 18884) | Novel Protein sim. GBank gi 3915488 sp O34961 YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION | | UNCLASSIFIED | 1006, 1016, 1022, 1027, 1034, 1039 |
| 3957 | 79837693 (8737, 8738) | Novel Protein sim. GBank gi 3915493 sp O68826 YIGM_PSEAE - HYPOTHETICAL 31.7 KD PROTEIN IN PHEC-RARD INTERGENIC REGION | | UNCLASSIFIED | 1008 |
| 3958 | 10249385 (5921, 5922) | Novel Protein sim. GBank gi 3915570 sp O34553 YTSP_BACSU - HYPOTHETICAL 8.7 KD PROTEIN IN BRAB-RPSD INTERGENIC REGION | | UNCLASSIFIED | 1023 |

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| 3959 | 80488988 (13693) 13694) | Novel Protein sim. GBank gi 3915659 sp Q10671 [COBL_MYCTU - PRECORRIN-6Y C5,15-METHYLTRANSFERASE - [DECARBOXYLATING] (PRECORRIN-6 METHYLTRANSFERASE) (PRECORRIN-6Y METHYLASE) | | UNCLASSIFIED | 1001, 1004, 1006, 1010, 1012, 1017, 1026, 1027, 1031, 1034, 1039, 1044 |
| 3960 | 20617394 (18129, 18130) | Novel Protein sim. GBank gi 3915993 sp P76250 YEAT_ECOLI - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN GAPA-RND INTERGENIC REGION | | UNCLASSIFIED | 1004 |
| 3961 | 79612824 (10109, 10110) | Novel Protein sim. GBank gi 3924708 emb CAA84646 - {Z35597} Weak similarity with sea squirt nidogen precursor protein (blastp score 7); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMBL... | | UNCLASSIFIED | 1022 |
| 3962 | 78499068 (7771, 7772) | Novel Protein sim. GBank gi 3928150 emb CAA10289 - {AJ131049} hypothetical protein [Cicer arietinum] | | UNCLASSIFIED | 1016 |
| 3963 | 79868855 (16225, 16226) | Novel Protein sim. GBank gi 3928723 emb CAA22219 - {AL034355} putative ABC transporter [Streptomyces coelicolor] | | UNCLASSIFIED | 1029, 1038 |
| 3964 | 80080052 (2403, 2404) | Novel Protein sim. GBank gi 3928904 (AF104259) - D-lysine 5,6-aminomutase alpha subunit [Clostridium sticklandii] | | UNCLASSIFIED | 1026, 1029, 1034, 1053 |
| 3965 | 78505129 (22979, 22980) | Novel Protein sim. GBank gi 3929019 (AF057695) - putative phosphotransmethylase [Haemophilus ducreyi] | | UNCLASSIFIED | 1022 |
| 3966 | 5731182 (17825, 17826) | Novel Protein sim. GBank gi 3935181 (AC004557) - F17L21.24 [Arabidopsis thaliana] | | UNCLASSIFIED | 1058 |

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| 3967 | 11348438 (19659, 19660) | Novel Protein sim. GBank gi 3953516 dbj BA34771 - (AB002529) sensor kinase ripA [Pseudomonas tolæsii] | UNCLASSIFIED | 1034 |
| 3968 | 36990483 (11115, 11116) | Novel Protein sim. GBank gi 395513 emb CAA05105 - (AJ010393) hypothetical protein [Pseudomonas oleovorans] | UNCLASSIFIED | 1016 |
| 3969 | 78723682 (269, 270) | Novel Protein sim. GBank gi 3978464 (AF065693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus] | UNCLASSIFIED | 1030 |
| 3970 | 23329490 (4905, 4906) | Novel Protein sim. GBank gi 3978488 (AF092918) - virulence regulating homolog [Pseudomonas alcaligenes] | UNCLASSIFIED | 1026 |
| 3971 | 36996970 (12591, 12592) | Novel Protein sim. GBank gi 3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana] | UNCLASSIFIED | 1001 |
| 3972 | 27976344 (9353, 9354) | Novel Protein sim. GBank gi 3986770 (AF109906) - NG2 [Mus musculus] | UNCLASSIFIED | 1024 |
| 3973 | 78913805 (18075, 18076) | Novel Protein sim. GBank gi 3990061 sp Q02336 ADA2_YEAST - POTENTIAL TRANSCRIPTIONAL ADAPTOR | UNCLASSIFIED | 1044 |
| 3974 | 66398162 (15901, 15902) | Novel Protein sim. GBank gi 399378 sp P31080 LEXA_BACSU - SOS REGULATORY PROTEIN LEXA_DINR | UNCLASSIFIED | 1008 |
| 3975 | 79470555 (18283, 18284) | Novel Protein sim. GBank gi 39980 sp P28155 HYPB_RHILV - HYDROGENASE EXPRESSION/FORMATION PROTEIN HYPB | UNCLASSIFIED | 1022 |
| 3976 | 29018958 (8735, 8736) | Novel Protein sim. GBank gi 400052 sp Q02138 LYC_LACLA - KETOL - ACID REDUCTOISOMERASE | UNCLASSIFIED | 1017 |
| 3977 | 20711888 (20917, 20918) | (ACETOHYDROXY-ACID ISOMEROREDUCTASE) (ALPHA-KETO-BETA- HYDROXYLACIL REDUCTOISOMERASE) | UNCLASSIFIED | 1022 |
| | | Novel Protein sim. GBank gi 400024 sp P31179 NADA_CYAPA - QUINOLINATE SYNTHETASE A | | |

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| 3978 | 27823479 (9323, 9324) | Novel Protein sim. GBank gi 400663 sp P31755 OCH1_YEAST - ALPHA-1,6-MANNOSYLTRANSFERASE | | UNCLASSIFIED | 1004, 1022, 1024, 1034 |
| 3979 | 80439852 (17195, 17196) | Novel Protein sim. GBank gi 4007381 emb CAA22367 - (AL034443) putative integral membrane transporter [Streptomyces coelicolor] | | UNCLASSIFIED | 1038 |
| 3980 | 65469531 (21673, 21674) | Novel Protein sim. GBank gi 4007726 emb CAA22410 - (AL034447) putative methylase [Streptomyces coelicolor] | | UNCLASSIFIED | 1008 |
| 3981 | 78923067 (11683, 11684) | Novel Protein sim. GBank gi 4007736 emb CAA22420 - (AL034447) putative chromosome associated protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1017 |
| 3982 | 25259598 (14463, 14464) | Novel Protein sim. GBank gi 4007738 emb CAA22422 - (AL034447) putative transmembrane protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1008 |
| 3983 | 78367994 (35, 36) | Novel Protein sim. GBank gi 4008343 emb CAB16307.1 - (Z99169) C26H9A.2 [Caenorhabditis elegans] | | UNCLASSIFIED | 1003 |
| 3984 | 65680443 (781, 782) | Novel Protein sim. GBank gi 401469 sp P28635 YAEC_ECOLI - HYPOTHETICAL 29.4 KD LIPOPROTEIN IN RCSF-ABC INTERGENIC REGION PRECURSOR | | UNCLASSIFIED | 1041 |
| 3985 | 78926497 (2677, 2678) | Novel Protein sim. GBank gi 401521 sp Q01334 YCR3_ERWHE - HYPOTHETICAL 29.9 KD PROTEIN IN CRTE 3 REGION (ORF3) | | UNCLASSIFIED | 1039 |
| 3986 | 79485919 (18921, 18922) | Novel Protein sim. GBank gi 403171 L24492 - ethanolamine ammonia-lyase large subunit [Rhodococcus erythropolis] | | UNCLASSIFIED | 1022 |
| 3987 | 80080258 (549, 550) | Novel Protein sim. GBank gi 4033729 (AF038595) - apolipoprotein N-acetyltransferase [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1027, 1031, 1034 |

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| 3988 | 32420106 (16625, 16626) | Novel Protein sim. GBank gil403406 (U00100) - unknown [Pseudomonas aeruginosa] | UNCLASSIFIED | 1029 |
| 3989 | 85543977 (21461, 21462) | Novel Protein sim. GBank gil403460 (L24521) - transformation-related protein [Homo sapiens] | UNCLASSIFIED | 1008, 1030, 1054 |
| 3990 | 78380848 (21147, 21148) | Novel Protein sim. GBank gil404524[bb136180 - (S64520) pyruvate: ferredoxin oxidoreductase [Anabaena variabilis], Peptide Partial, 91 aa] [Anabaena variabilis] | UNCLASSIFIED | 1026 |
| 3991 | 16316610 (18763, 18764) | Novel Protein sim. GBank gil404817 (L24780) - suppressor [Saccharomyces cerevisiae] | UNCLASSIFIED | 1001 |
| 3992 | 80027600 (7055, 7056) | Novel Protein sim. GBank gil4049524[emb CAA10483] - (AJ131707) fructose 1,6-bisphosphate adolase [Streptomyces galbus] | UNCLASSIFIED | 1004, 1006, 1009, 1023, 1038 |
| 3993 | 20629923 (6413, 6414) | Novel Protein sim. GBank gil4050089 (AF109907) - hypothetical protein [Homo sapiens] | UNCLASSIFIED | 1010 |
| 3994 | 78758003 (18967, 18968) | Novel Protein sim. GBank gil4056551[emb CAA22586] - (AL034583) putative elongation initiation factor subunit [Schizosaccharomyces pombe] | UNCLASSIFIED | 1030 |
| 3995 | 79245937 (1369, 1370) | Novel rProtein sim. GBank gil405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli] | UNCLASSIFIED | 1039 |
| 3996 | 17939614 (309, 310) | Novel rProtein sim. GBank gil4062973[dbj BA36204.1] - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida] | UNCLASSIFIED | 1039 |
| 3997 | 5631925 (22675, 22676) | Novel Protein sim. GBank gil4092859 (AF033120) - p53 regulated PA26-T2 nuclear protein [Homo sapiens] | UNCLASSIFIED | 1058 |
| 3998 | 56001677 (4235, 4236) | Novel Protein sim. GBank gil4098081 (U733336) - anaerobic ribonucleotide reductase [Lactococcus lactis] | UNCLASSIFIED | 1003 |
| 3999 | 11695413 (1851, 1852) | Novel Protein sim. GBank gil4104762[gb AAD02144.1] - (AF039534) transposase-like protein TnpA2 [Pseudomonas stutzeri] | UNCLASSIFIED | 1006 |

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| 4000 | 79761420 (11707, 11708) | Novel Protein sim. GBank gil4104925 (AF042276) - poly(hydroxyalcanoate) granule associated protein Cia2 [Pseudomonas putida] | | UNCLASSIFIED | |
| 4001 | 79398200 (20263, 20264) | Novel Protein sim. GBank gil4106577[lemb CAA21332] - (AL031866) ORF10, len: 268 aa, hutG, highly similar to N-formylglutamate amidohydrolase, from Pseudomonas putida AF032970, 3, Fasta scores: opt: 1057, E(): 0, 59.6% identity in 260 aa overlap [Yersinia pestis] | | UNCLASSIFIED | 1006 |
| 4002 | 81809267 (617, 618) | Novel Protein sim. GBank gil4106587[lemb CAA21342] - (AL031866) ORF19, len: 473 aa, similar to tyrosine aminotransferase, highly similar to E. coli D90784, 2, Fasta scores opt: 1842, E(): 0 [Yersinia pestis] | | UNCLASSIFIED | 1012, 1054 |
| 4003 | 36827630 (5481, 5482) | Novel Protein sim. GBank gil4106610[lemb CAA21365] - (AL031866) ORF42, len=386 aa , similarity to an aminotransferase, In P95957 Sulfolobus solfataricus, (401 aa), 33,1% identity in 393 aa overlap, Fasta scores: opt:468, E(): 8.5e-24, in Q64602 R. norvegicus,(425 aa), 28.6% ident... | | UNCLASSIFIED | 1054 |
| 4004 | 79489610 (19187, 19188) | Novel Protein sim. GBank gil4106613[lemb CAA21368] - (AL031866) ORF45, len= 289 aa, unknown [Yersinia pestis] | | UNCLASSIFIED | 1022 |
| 4005 | 10812585 (14111, 14112) | Novel Protein sim. GBank gil4115383 (AC005967) - receptor-like protein kinase [Arabidopsis thaliana] | | UNCLASSIFIED | 1034 |
| 4006 | 14995589 (16631, 16632) | Novel Protein sim. GBank gil4115511[dbj BAA36399_1] - (AB010947) FfY [Salmonella typhimurium] | | UNCLASSIFIED | 1024 |
| 4007 | 79846553 (12761, 12762) | Novel Protein sim. GBank gil4115631[dbj BAA36469] - (AB015053) ORFX; unassigned reading frame [Pseudomonas fluorescens] | | UNCLASSIFIED | 1039 |

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| 4008 | 79249976 (1921, 1922) | Novel Protein sim. GBank gi 4128215 (AF095748) - putative phathalate permease C-terminal region [Burkholderia cepacia] | UNCLASSIFIED | 1001 |
| 4009 | 79610551 (4565, 4566) | Novel Protein sim. GBank gi 4154082 emb CAA22735 - (AL035161) putative aminoacylase [Streptomyces coelicolor] | UNCLASSIFIED | 1004, 1041 |
| 4010 | 91014288 (1491, 1492) | Novel Protein sim. GBank gi 4155340 (AE001508) - TYPE I RESTRICTION ENZYME (RESTRICTION SUBUNIT) [Helicobacter pylori] J99] | UNCLASSIFIED | 1010 |
| 4011 | 66376543 (10897, 10898) | Novel Protein sim. GBank gi 4155544 (AE001525) - putative POLYSACCHARIDE BIOSYNTHESIS PROTEIN [Helicobacter pylori] J99] | UNCLASSIFIED | 1009, 1010 |
| 4012 | 80209497 (11793, 11794) | Novel Protein sim. GBank gi 4155633 (AE001532) - putative [Helicobacter pylori] J99] | UNCLASSIFIED | 1034 |
| 4013 | 10857039 (325, 326) | Novel Protein sim. GBank gi 4155750 (AE001542) - D-LACTATE DEHYDROGENASE [Helicobacter pylori] J99] | UNCLASSIFIED | 1006 |
| 4014 | 80209512 (16981, 16982) | Novel Protein sim. GBank gi 4155868 (AE001549) - putative tRNA (5-METHYLMINOMETHYL-2'- THIOURIDYLATE)-METHYLTRANSFERASE [Helicobacter pylori] J99] | UNCLASSIFIED | 1034 |
| 4015 | 13886417 (15477, 15478) | Novel Protein sim. GBank gi 4155870 (AE001549) - putative [Helicobacter pylori] J99] | UNCLASSIFIED | 1053 |
| 4016 | 142118589 (12173, 12174) | Novel Protein sim. GBank gi 4155916 (AE001554) - lipopolysaccharide biosynthesis protein [Helicobacter pylori] J99] | UNCLASSIFIED | 1053 |
| 4017 | 79107407 (14345, 14346) | Novel Protein sim. GBank gi 4156196 (AC004865) - similar to KIAA0319; similar to AB002317 (PID:92224579) [Homo sapiens] | UNCLASSIFIED | 1023 |
| 4018 | 25267792 (3601, 3602) | Novel Protein sim. GBank gi 4160312 emb CAA22783 - (AL035212) hypothetical protein SC9B2.03 [Streptomyces coelicolor] | UNCLASSIFIED | 1003 |

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| 4019 | 20753820 (17145, 17146) | Novel Protein sim. GBank q 416583 sp P27550 ACSA_ECOLI - ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME) | UNCLASSIFIED | 1004 |
| 4020 | 80235985 (1607, 1608) | Novel Protein sim. GBank q 416582 sp P32333 AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR | UNCLASSIFIED | 1006, 1023 |
| 4021 | 85806685 (16071, 16072) | Novel Protein sim. GBank q 416582 sp P32333 AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR | UNCLASSIFIED | 1017, 1019, 1026, 1053, 1054 |
| 4022 | 79611262 (2165, 2166) | Novel Protein sim. GBank q 416761 sp P32468 CC12_YEAST - CELL DIVISION CONTROL PROTEIN 12 (SEPTIN) | UNCLASSIFIED | 1001, 1006, 1044 |
| 4023 | 80227710 (21229, 21230) | Novel Protein sim. GBank q 417039 sp Q01722 GCR2_YEAST - GLYCOLYTIC GENES TRANSCRIPTIONAL ACTIVATOR GCR2 | UNCLASSIFIED | 1006, 1022, 1034 |
| 4024 | 65454473 (11741, 11742) | Novel Protein sim. GBank q 417226 sp P32895 KPR1_YEAST - RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1) | UNCLASSIFIED | 1016, 1022 |
| 4025 | 47652453 (12005, 12006) | Novel Protein sim. GBank q 417315 sp P32653 MRP_STRSU - MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KD SURFACE PROTEIN) | UNCLASSIFIED | 1029 |
| 4026 | 78728468 (9511, 9512) | Novel Protein sim. GBank q 417457 sp P32767 PDR6_YEAST - PLEIOTROPIC DRUG RESISTANCE REGULATORY PROTEIN 6 | UNCLASSIFIED | 1008, 1009, 1017, 1022, 1026, 1039, 1044 |
| 4027 | 25262406 (12921, 12922) | Novel Protein sim. GBank q 4176522 emb CAA228781 - (AL035263) hypothetical protein [Schizosaccharomyces pombe] | UNCLASSIFIED | 1008 |

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| 4028 | 95292770 (21653, 21654) | Novel Protein sim. GBank gil417770isp P32432 SFP1_YEAST - ZINC FINGER PROTEIN SFP1 | | UNCLASSIFIED | 1004 |
| 4029 | 80279785 (5281, 5282) | Novel Protein sim. GBank gil417778isp P32908 SMC1_YEAST - CHROMOSOME SEGREGATION PROTEIN SMC1 (DA-BOX PROTEIN SMC1) | | UNCLASSIFIED | 1006, 1008, 1010, 1024, 1027, 1031 |
| 4030 | 30660836 (12051, 12052) | Novel Protein sim. GBank gil417826isp P32579 SUA5_YEAST - SUA5 PROTEIN | | UNCLASSIFIED | 1026 |
| 4031 | 37789306 (12211, 12212) | Novel Protein sim. GBank gil418384isp P32057 WCAL_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAL | | UNCLASSIFIED | 1012 |
| 4032 | 29449853 (21729, 21730) | Novel Protein sim. GBank gil418427isp P32634 YEW2_YEAST - HYPOTHETICAL 195.4 KD PROTEIN IN RPS26B-GLC7 INTERGENIC REGION | | UNCLASSIFIED | 1026 |
| 4033 | 80042837 (5815, 5816) | Novel Protein sim. GBank gil418488isp P32147 YIHZ_ECOLI - HYPOTHETICAL 15.9 KD PROTEIN IN RBN-FDHE INTERGENIC REGION (O145) | | UNCLASSIFIED | 1053 |
| 4034 | 9333442 (9203, 9204) | Novel Protein sim. GBank gil4185011isp P32159 YIIP_ECOLI - HYPOTHETICAL 32.9 KD PROTEIN IN CPXA-PFKA INTERGENIC REGION | | UNCLASSIFIED | 1017 |
| 4035 | 8490783 (2585, 2586) | Novel Protein sim. GBank gil418572isp P322862 YKD8_YEAST - PUTATIVE 128.2 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN PTM1-JXR1 INTERGENIC REGION | | UNCLASSIFIED | 1024 |
| 4036 | 56749063 (7345, 7346) | Novel Protein sim. GBank gil4186001isp P322792 YHH7_YEAST - HYPOTHETICAL 44.2 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION | | UNCLASSIFIED | 1003 |

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| 4037 | 30198359 (7755, 7756) | Novel Protein sim. GBank gi 419481 pir A46312 - gag polyprotein - human endogenous virus S71 | | UNCLASSIFIED | 1026 |
| 4038 | 38615868 (4941, 4942) | Novel Protein sim. GBank gi 419757 pir S30145 - ketol-acid reductoisomerase (EC 1.1.1.86) precursor - Arabidopsis thaliana | | UNCLASSIFIED | 1008, 1025 |
| 4039 | 94664584 (22829, 22830) | Novel Protein sim. GBank gi 419857 pir S34027 - CDC47 protein - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1010 |
| 4040 | 28786675 (19377, 19378) | Novel Protein sim. GBank gi 4204263 (AC005223) - 40409 [Arabidopsis thaliana] | | UNCLASSIFIED | 1017 |
| 4041 | 94233665 (18313, 18314) | Novel Protein sim. GBank gi 4204265 (AC005223) - 45643 [Arabidopsis thaliana] | | UNCLASSIFIED | 1003, 1004 |
| 4042 | 20024135 (22073, 22074) | Novel Protein sim. GBank gi 4204304 (AC003027) - 101 pir _seq No definition line found [Arabidopsis thaliana] | | UNCLASSIFIED | 1010 |
| 4043 | 10368203 (16661, 16662) | Novel Protein sim. GBank gi 4204747 (U49838) - 72.2 kDa protein [Mycobacterium leprae] | | UNCLASSIFIED | 1008 |
| 4044 | 79207699 (14799, 14800) | Novel Protein sim. GBank gi 4206763 (AF04328) - cell wall plasma membrane linker protein homolog [Arabidopsis thaliana] | | UNCLASSIFIED | 1001 |
| 4045 | 20724578 (5729, 5730) | Novel Protein sim. GBank gi 420945 pir A47041 - transposase homolog (Insertion element I SAE1) - Alcaligenes eutrophus | | UNCLASSIFIED | 1006 |
| 4046 | 17932141 (18111, 18112) | Novel Protein sim. GBank gi 421091 pir S30730 - hypothetical protein o206 - Escherichia coli | | UNCLASSIFIED | 1023 |
| 4047 | 10887336 (9541, 9542) | Novel Protein sim. GBank gi 42144 pir CAA25200 - (X00513) NusA protein (nusA) [Escherichia coli] | | UNCLASSIFIED | 1027 |
| 4048 | 87461732 (17329, 17330) | Novel Protein sim. GBank gi 4220517 pir CAA22990 - (AL035356) hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1025 |

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| 4049 | 8518032 (21319, 21320) | Novel Protein sim. GBank gi 4220523 emb CAA22996 - (AL035356) putative allin lyase [Arabidopsis thaliana] | | UNCLASSIFIED | 1022 |
| 4050 | 20294766 (9587, 9588) | Novel Protein sim. GBank gi 4234790 (AF078736) - unknown [Leptospira borgpetersenii] | | UNCLASSIFIED | 1034 |
| 4051 | 29481334 (2687, 2688) | Novel Protein sim. GBank gi 423565 pir S34583 - serine proteinase (EC 3.4.21.-) PC6B - mouse | | UNCLASSIFIED | 1038 |
| 4052 | 10115867 (2855, 2856) | Novel Protein sim. GBank gi 4240195 dbj BAA74876.1 - (AB020660) KIAA0853 protein [Homo sapiens] | | UNCLASSIFIED | 1017 |
| 4053 | 20598367 (13221, 13222) | Novel Protein sim. GBank gi 4240195 dbj BAA74876.1 - (AB020660) KIAA0853 protein [Homo sapiens] | | UNCLASSIFIED | 1022 |
| 4054 | 57291915 (21019, 21020) | Novel Protein sim. GBank gi 42413239 dbj BAA74898.1 - (AB020682) KIAA0875 protein [Homo sapiens] | | UNCLASSIFIED | 1010 |
| 4055 | 78674809 (13125, 13126) | Novel Protein sim. GBank gi 4263695 gb AAD15381 - (AC006223) putative myosin II heavy chain [Arabidopsis thaliana] | | UNCLASSIFIED | 1009 |
| 4056 | 29242471 (3935, 3936) | Novel Protein sim. GBank gi 4320 emb CAA36300 - (X52081) RGP1 (reduced growth phenotype) gene product (AA 1-661) [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1017 |
| 4057 | 11698120 (2559, 2560) | Novel Protein sim. GBank gi 4322011 gb AAD15914 - (AF069392) polar flagellar assembly protein [Vibrio parahaemolyticus] | | UNCLASSIFIED | 1031 |
| 4058 | 55997711 (2417, 2418) | Novel Protein sim. GBank gi 432498 (L26506) - ZMS1 [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1003 |

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| 4059 | 28301995 (14846) 14846) | Novel Protein sim. GBank g 4325346 gb AAD17345 - (AF128393) similar to N-ethylmaleimide sensitive fusion proteins; contains similarity to ATPases (Pfam: PF00004, Score=307.7, E=1.4e-88n N=1) [Arabidopsis thaliana] | | UNCLASSIFIED | 1017 |
| 4060 | 27364469 (18132) 18132) | Novel Protein sim. GBank g 43281em b CAA47121 - (X66501) RIF1 [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1022 |
| 4061 | 10855157 (6137, 6138) | Novel Protein sim. GBank g 4336800 gb AAD17959 - (AF106002) toluene tolerance protein Tt22C [Pseudomonas putida] | | UNCLASSIFIED | 1031 |
| 4062 | 39710928 (13657, 13658) | Novel Protein sim. GBank g 4337174 gb AAD18085 - (AC006416) Similar to g 1573829 H 0816 aminopeptidase P-homolog (pepP) from Haemophilus influenzae genome gb U32764 [Arabidopsis thaliana] | | UNCLASSIFIED | 1026 |
| 4063 | 1074167 (7909, 7910) | Novel Protein sim. GBank g 4371280 gb AAD18138 - (AC006260) hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1004 |
| 4064 | 29685014 (15419, 15420) | Novel Protein sim. GBank g 437f670 gb AAD18535 - (AE001623) dCTP Deaminase [Chlamydia pneumoniae] | | UNCLASSIFIED | 1038 |
| 4065 | 10331900 (20469, 20470) | Novel Protein sim. GBank g 4377312 gb AAD19121 - (AE001679) Ribonucleoside Reductase, Large Chain [Chlamydia pneumoniae] | | UNCLASSIFIED | 1003 |
| 4066 | 34868401 (17955, 17956) | Novel Protein sim. GBank g 4388730 gb AAD19768 - (AC006413) hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1034 |
| 4067 | 85526859 (20389, 20390) | Novel Protein sim. GBank g 4406775 gb AAD20086 - (AC006836) unknown protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1049 |
| 4068 | 16395460 (20235, 20236) | Novel Protein sim. GBank g 4416478 gb AAD20378 - (AF125999) transposase [Mycobacterium avium] | | UNCLASSIFIED | 1017 |

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| 4069 | 79202004 (13603, 13604) | Novel Protein sim. GBank gil4455098[gb]AAD21076] - (AF121797) AG-specific adenine glycosylase [Streptomyces antibioticus] | | UNCLASSIFIED | 1024 |
| 4070 | 25143281 (15063, 15064) | Novel Protein sim. GBank gil4455367[emb CAB36777.1] - (AL035524) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1003 |
| 4071 | 8208833 (18665, 18666) | Novel Protein sim. GBank gil4455367[emb CAB36777.1] - (AL035524) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1022 |
| 4072 | 49127474 (10057, 10058) | Novel Protein sim. GBank gil4455767[emb CAB36883] - (AL035537) hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1040 |
| 4073 | 65691754 (971, 972) | Novel Protein sim. GBank gil4467129[emb CAB37560] - (AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana] | | UNCLASSIFIED | 1009 |
| 4074 | 71761719 (1441, 1442) | Novel Protein sim. GBank gil4467249[emb CAB37574] - (AL035569) probable Glu-tRNAGln amidotransferase subunit C [Streptomyces coelicolor] | | UNCLASSIFIED | 1008, 1026 |
| 4075 | 35904710 (159, 160) | Novel Protein sim. GBank gil4467252[emb CAB37577] - (AL035569) probable Glu-tRNAGln amidotransferase subunit B [Streptomyces coelicolor] | | UNCLASSIFIED | 1029 |
| 4076 | 33205246 (13817, 13818) | Novel Protein sim. GBank gil4467252[emb CAB37577] - (AL035569) probable Glu-tRNAGln amidotransferase subunit B [Streptomyces coelicolor] | | UNCLASSIFIED | 1026 |
| 4077 | 80248876 (18671, 18672) | Novel Protein sim. GBank gil4490579[emb CAB38729.1] - (AJ010302) mg protoporphyrin IX monomethyl ester oxidative cyclase subunit [Rhodobacter sphaeroides] | | UNCLASSIFIED | 1006, 1022 |

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| 4078 | 80173375 (20561, 20562) | Novel Protein sim. GBank gi 4494921 gb AAD21343.1 - (AF083501) capsid protein [Macaca mulatta rhadinivirus 17577] | | |
| 4079 | 79833783 (11355, 11356) | Novel Protein sim. GBank gi 4502245 ref NP_003867.1 pARTN - neurotoxic factor artemin precursor | UNCLASSIFIED | 1008 |
| 4080 | 83220998 (4723, 4724) | Novel Protein sim. GBank gi 4503275 ref NP_001913.1 pDCtI - dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) | UNCLASSIFIED | 1028 |
| 4081 | 94673275 (6111, 6112) | Novel Protein sim. GBank gi 4503895 ref NP_000145.1 pGALK - galactokinase 1 | UNCLASSIFIED | 1031 |
| 4082 | 78389465 (9099, 9100) | Novel Protein sim. GBank gi 4504525 ref NP_003962.1 pHS1 - UNKNOWN | UNCLASSIFIED | 1008 |
| 4083 | 3057723 (15791, 15792) | Novel Protein sim. GBank gi 4506133 ref NP_002779.1 pPSMA - proteasome (prosome, macropain) subunit, alpha type 3 | UNCLASSIFIED | 1009 |
| 4084 | 46892345 (12117, 12118) | Novel Protein sim. GBank gi 4506545 ref NP_002923.1 pRMSA - regulator of mitotic spindle assembly 1 | UNCLASSIFIED | 1042 |
| 4085 | 78728876 (17701, 17702) | Novel Protein sim. GBank gi 4510347 gb AAD21436.1 - (AC006921) hypothetical protein [Arabidopsis thaliana] | UNCLASSIFIED | 1022, 1053 |
| 4086 | 37028556 (14485, 14486) | Novel Protein sim. GBank gi 4511974 gb AAD21534.1 - (AF088896) unknown [Zymomonas mobilis] | UNCLASSIFIED | 1038 |
| 4087 | 29354727 (16987, 16988) | Novel Protein sim. GBank gi 4512242 dbj BAA75236.1 - (AB014750) polyprotein [Nicotiana tabacum] | UNCLASSIFIED | 1008 |
| 4088 | 79877933 (17547, 17548) | Novel Protein sim. GBank gi 4512377 dbj BAA75341.1 - (AB011837) sorbitol dehydrogenase [Bacillus halodurans] | UNCLASSIFIED | 1001, 1003, 1006, 1012, 1017, 1024, 1026, 1027, 1031 |

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| 4089 | 35933724 (20725, 20726) | Novel Protein sim. GBank gi 4512492 dbj BAA75141.1 - (AB021078) 100 pct identical to gp.STY1NC1 PR_5_pf220934eE TrBC of plasmid R641 [Plasmid Colib-P9] | | |
| 4090 | 21629494 (9909, 9910) | Novel Protein sim. GBank gi 4512671 gb AAD21725.1 - (AC006931) unknown protein [Arabidopsis thaliana] | UNCLASSIFIED | 1001 |
| 4091 | 20298627 (2717, 2718) | Novel Protein sim. GBank gi 4539105 emb CAB39826.1 - (AL049491) putative ATP-binding protein [Mycobacterium leprae] | UNCLASSIFIED | 1034 |
| 4092 | 78787745 (12651, 12652) | Novel Protein sim. GBank gi 4539105 emb CAB39826.1 - (AL049491) putative ATP-binding protein [Mycobacterium leprae] | UNCLASSIFIED | 1017, 1049 |
| 4093 | 20727978 (17891, 17892) | Novel Protein sim. GBank gi 4539193 emb CAB39722.1 - (AL049485) putative fatty oxidation protein [Streptomyces coelicolor] | UNCLASSIFIED | 1006 |
| 4094 | 20715521 (17865, 17866) | Novel Protein sim. GBank gi 4539223 emb CAB39881.1 - (AL049497) putative integral membrane protein [Streptomyces coelicolor] | UNCLASSIFIED | 1022, 1039 |
| 4095 | 23285736 (1515, 1516) | Novel Protein sim. GBank gi 4539292 emb CAB39595.1 - (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] | UNCLASSIFIED | 1008 |
| 4096 | 14996508 (6603, 6604) | Novel Protein sim. GBank gi 4539383 emb CAB37449.1 - (AL035526) putative protein (fragment) [Arabidopsis thaliana] | UNCLASSIFIED | 1024 |
| 4097 | 10173729 (8125, 8126) | Novel Protein sim. GBank gi 4539386 emb CAB37452.1 - (AL035526) extensin-like protein [Arabidopsis thaliana] | UNCLASSIFIED | 1004 |

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| 4098 | 78956879 (17899, 17900) | Novel Protein sim. GBank gi 4539386 emb CAB37452.1 - (AL035526) extensin-like protein [Arabidopsis thaliana] | UNCLASSIFIED | 1054 |
| 4099 | 16329416 (18739, 18740) | Novel Protein sim. GBank gi 4539386 emb CAB37452.1 - (AL035526) extensin-like protein [Arabidopsis thaliana] | UNCLASSIFIED | 1004 |
| 4100 | 47656627 (3953, 3954) | Novel Protein sim. GBank gi 4539532 emb CAB38501.1 - (AL035636) putative sodium/proton antiporter [Streptomyces coelicolor] | UNCLASSIFIED | 1029 |
| 4101 | 66694242 (5915, 5916) | Novel Protein sim. GBank gi 4539532 emb CAB38501.1 - (AL035636) putative sodium/proton antiporter [Streptomyces coelicolor] | UNCLASSIFIED | 1009 |
| 4102 | 20463731 (6383, 6384) | Novel Protein sim. GBank gi 4545228 gb AAD22450.1 AF11618 - (AF116183) SecA homolog [Actinobacillus actino myceliumcomitans] | UNCLASSIFIED | 1010 |
| 4103 | 9845416 (2423, 2424) | Novel Protein sim. GBank gi 4545223 gb AAD22455.1 AF11628 - (AF116284) unknown [Pseudomonas aeruginosa] | UNCLASSIFIED | 1023 |
| 4104 | 66051487 (8739, 8740) | Novel Protein sim. GBank gi 4545231 gb AAD22455.1 AF11628 - (AF116284) unknown [Pseudomonas aeruginosa] | UNCLASSIFIED | 1010 |
| 4105 | 9398483 (855, 856) | Novel Protein sim. GBank gi 456720 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana] | UNCLASSIFIED | 1017 |
| 4106 | 23332081 (18767, 18768) | Novel Protein sim. GBank gi 4580470 gb AAD24394.1 AC00608 - (AC006081) hypothetical protein [Arabidopsis thaliana] | UNCLASSIFIED | 1053 |

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| 4107 | 80226635 (11291, 11292) | Novel Protein sim. GBank g 14581504 emb CAB40163.1 - (AL049558) hypothetical protein [Schizosaccharomyces pombe] | UNCLASSIFIED | 1006, 1010, 1024, 1027 |
| 4108 | 55004686 (751, 752) | Novel Protein sim. GBank g 14583397 gb AAD25061.1 /AF12100 - (AF12100) S1628 transposase TnpB [Connebacterium glutamicum] | UNCLASSIFIED | 1019 |
| 4109 | 79605200 (9623, 9624) | Novel Protein sim. GBank g 14583559 emb CAB40368.1 - (AJ005255) OxyR [Erwinia chrysanthemi] | UNCLASSIFIED | 1034 |
| 4110 | 57147813 (14547, 14548) | Novel Protein sim. GBank g 1458420 (U06451) - proline permease homolog [Staphylococcus aureus] | UNCLASSIFIED | 1004 |
| 4111 | 78916292 (5757, 5758) | Novel Protein sim. GBank g 14584420 emb CAB40740.1 - (AJ011317) Orf361 [Lactobacillus sp. CM4] | UNCLASSIFIED | 1039 |
| 4112 | 79875001 (19585, 19586) | Novel Protein sim. GBank g 14584438 emb CAB40701.1 - (AL049587) putative efflux protein [Streptomyces coelicolor] | UNCLASSIFIED | 1017 |
| 4113 | 78764485 (14933, 14934) | Novel Protein sim. GBank g 14584527 emb CAB40758.1 - (AL049607) putative protein [Arabidopsis thaliana] | UNCLASSIFIED | 1039 |
| 4114 | 79868279 (7851, 7852) | Novel Protein sim. GBank g 14584539 emb CAB40769.1 - (AL049608) extensin-like protein [Arabidopsis thaliana] | UNCLASSIFIED | 1025, 1031 |
| 4115 | 20177089 (19655, 19656) | Novel Protein sim. GBank g 14585587 emb CAB40855.1 - (AL049628) putative adenosine glycosylase [Streptomyces coelicolor] | UNCLASSIFIED | 1010 |
| 4116 | 29912055 (6877, 6878) | Novel Protein sim. GBank g 14586963 dbj BA-A78556.1 - (AB018253) voltage-gated ca channel [Rattus norvegicus] | UNCLASSIFIED | 1022 |
| 4117 | 11287498 (7595, 7596) | Novel Protein sim. GBank g 14587313 dbj BAA76709.1 - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90] | UNCLASSIFIED | 1022 |

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| 4118 | 66727941 (18969, 18970) | Novel Protein sim. GBank gij4587326[dbj BAA76717.1] - (AB025424) aconitase [Corynebacterium glutamicum] | | UNCLASSIFIED | 1009 |
| 4119 | 78735337 (4713, 4714) | Novel Protein sim. GBank gij4587571[gb AAD25802.1 AC006555 - (AC006550) Belongs to the PF 01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana] | | UNCLASSIFIED | 1008 |
| 4120 | 8504857 (20305, 20306) | Novel Protein sim. GBank gij4588130[gb AAD25997.1 AF110254 - (AF102548) AT1 receptor-associated protein [Mus musculus] | | UNCLASSIFIED | 1024 |
| 4121 | 19869742 (12611, 12612) | Novel Protein sim. GBank gij4589361[gb AAD26468.1] - (AF140505) DEAD box RNA helicase [Candida albicans] | | UNCLASSIFIED | 1022 |
| 4122 | 79613010 (6539, 6540) | Novel Protein sim. GBank gij4589484[dbj BAA76770.1] - (AB023143) KIAAC926 protein [Homo sapiens] | | UNCLASSIFIED | 1025 |
| 4123 | 20729925 (12773, 12774) | Novel Protein sim. GBank gij4589636[dbj BAA76840.1] - (AB023213) KIAAC996 protein [Homo sapiens] | | UNCLASSIFIED | 1004 |
| 4124 | 20465916 (6553, 6554) | Novel Protein sim. GBank gij460249 (U07228) - Saccharomyces cerevisiae Rev7p (REV7) gene, complete cds. [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1010, 1022 |
| 4125 | 80429246 (19267, 19268) | Novel Protein sim. GBank gij461402 (L29642) - methyltransferase [Pseudomonas fluorescens] | | UNCLASSIFIED | 1038 |
| 4126 | 79751472 (5807, 5808) | Novel Protein sim. GBank gij4616231[sp P29853 BGAL ASPNG - BETA- GALACTOSIDASE PRECURSOR (LACTASE) | | UNCLASSIFIED | 1003, 1004, 1009, 1054 |
| 4127 | 27962594 (9859, 9860) | Novel Protein sim. GBank gij4619151[sp P33894 DAP1 YEAST - DIPEPTIDYL AMINOPEPTIDASE A (DPAP A) (YSCIV)] | | UNCLASSIFIED | 1001, 1006, 1010, 1022, 1024, 1031, 1034 |

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| 4128 | 19882613 (21315, 21316) | Novel Protein sim. GBank gi 462168 sp P33892 GCN1_YEAST - TRANSLATIONAL ACTIVATOR GCN1 | UNCLASSIFIED | 1022 |
| 4129 | 81918276 (7487, 7488) | Novel Protein sim. GBank gi 462569 sp P34926 MAPA_RAT - MICROTUBULE-ASSOCIATED PROTEIN 1A (CONTAINS: LIGHT CHAIN LC2) | UNCLASSIFIED | 1054 |
| 4130 | 37809745 (11367, 11368) | Novel Protein sim. GBank gi 462569 sp P34926 MAPA_RAT - MICROTUBULE-ASSOCIATED PROTEIN 1A (CONTAINS: LIGHT CHAIN LC2) | UNCLASSIFIED | 1058 |
| 4131 | 27851045 (22447, 22448) | Novel Protein sim. GBank gi 462623 sp Q00587 MSE5_HUMAN - SERUM PROTEIN MSE55 | UNCLASSIFIED | 1006, 1022 |
| 4132 | 80478201 (2967, 2968) | Novel Protein sim. GBank gi 462560 sp P33412 MUQ1_YEAST - MUQ1 PROTEIN | UNCLASSIFIED | 1010, 1012, 1022, 1024 |
| 4133 | 16424704 (15095, 15096) | Novel Protein sim. GBank gi 463432 (U05214) - prolactinase [Lactobacillus helveticus] | UNCLASSIFIED | 1038 |
| 4134 | 78518093 (18819, 18820) | Novel Protein sim. GBank gi 464620 gb IAAD26879.1 AC00723 - (AC007230) Contains similarity to gb D13630 KIAA0005 gene from Homo sapiens. ESTs gb T45345, gb T21086, gb R90360, gb T20468, gb T45191 and gb A100459 come from this gene. [Arabidopsis thaliana] | UNCLASSIFIED | 1017 |
| 4135 | 20463398 (6699, 6700) | Novel Protein sim. GBank gi 464758 sp P33330 SERC_YEAST - PHOSPHOSERINE AMINO-TRANSFERASE (PSAT) | UNCLASSIFIED | 1010, 1017 |
| 4136 | 80231895 (4801, 4802) | Novel Protein sim. GBank gi 464800 sp P34164 SIP2_YEAST - SIP2 PROTEIN (SPM2 PROTEIN) | UNCLASSIFIED | 1008, 1022, 1024, 1025, 1026, 1031, 1038 |
| 4137 | 8368192 (75, 76) | Novel Protein sim. GBank gi 464826 sp P14825 SYK2_ECOLI - LYSYL-TRNA SYNTHETASE, HEAT INDUCIBLE (LYSINE-TRNA LIGASE) (LYSRS) | UNCLASSIFIED | 1022 |

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| 4138 | 79830712 (17289, 17290) | Novel Protein sim. GBank g 46781;37 emb CAB41210.1 - (AL049661) putative lipoprotein [Streptomyces coelicolor] | UNCLASSIFIED | 1039 |
| 4139 | 85800726 (14201, 14202) | Novel Protein sim. GBank g 4678899 emb CAB41271.1 - (AL049707) putative large glycine/alanine rich protein [Streptomyces coelicolor] | UNCLASSIFIED | 1025 |
| 4140 | 78891820 (8907, 8908) | Novel Protein sim. GBank g 4680651 gb AAD27712.1 AF13293 - (AF13293) CGI-02 protein [Homo sapiens] | UNCLASSIFIED | 1006, 1038 |
| 4141 | 30259427 (22745, 22746) | Novel Protein sim. GBank g 4680651 gb AAD27712.1 AF13293 - (AF13293) CGI-02 protein [Homo sapiens] | UNCLASSIFIED | 1008 |
| 4142 | 79844531 (21555, 21556) | Novel Protein sim. GBank g 4680671 gb AAD27725.1 AF13295 - (AF1325) CGI-16 protein [Homo sapiens] | UNCLASSIFIED | 1008 |
| 4143 | 56152827 (20579, 20580) | Novel Protein sim. GBank g 4691726 gb AAD28046.1 AF12449 - (AF12449) ARF GTPase-activating protein GIT1 [Homo : apiens] | UNCLASSIFIED | 1003 |
| 4144 | 28387803 (15615, 15616) | Novel Protein sim. GBank g 4725999 emb CAB41728.1 - (AL049731) putative transpeptidase [Streptomyces coelicolor] | UNCLASSIFIED | 1016 |
| 4145 | 85528995 (479, 480) | Novel Protein sim. GBank g 4753853 emb CAB42016.1 - (AL049754) putative adenylosuccinate synthetase [Streptomyces coelicolor] | UNCLASSIFIED | 1049 |
| 4146 | 20437227 (13685, 13686) | Novel Protein sim. GBank g 473871 emb CAB42034.1 - (AL049754) hypothetical protein [Streptomyces coelicolor] | UNCLASSIFIED | 1010 |
| 4147 | 16327929 (9021, 9022) | Novel Protein sim. GBank g 4737095 emb CAB42080.1 - (AL049763) conserved hypothetical protein [Streptomyces coelicolor] | UNCLASSIFIED | 1004 |

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| 4148 | 94324296 (13171, 13172) | Novel Protein sim. GBank g 4757846 ref NP_004317.1 pBCL9 - B-cell CLL lymphoma 9 | | UNCLASSIFIED | 1044 |
| 4149 | 58214305 (12441, 12442) | Novel Protein sim. GBank g 4733026 ref NP_004361.1 pCOL1 - collagen, type XI, alpha 1 | | UNCLASSIFIED | 1038 |
| 4150 | 81852285 (5527, 5528) | Novel Protein sim. GBank g 4761595 gb AAD29417.1 AF13195 - (AF131951) Shank1a [Rattus norvegicus] | | UNCLASSIFIED | 1010, 1054 |
| 4151 | 10253081 (4243, 4244) | Novel Protein sim. GBank g 476794 pir A40678 - T-cell adhesion receptor CD2 homolog - African swine fever virus | | UNCLASSIFIED | 1038 |
| 4152 | 80200962 (8715, 8716) | Novel Protein sim. GBank g 4768831 gb AAD29633.1 AF11682 - (AF113827) unknown [Homo sapiens] | | UNCLASSIFIED | 1022, 1034 |
| 4153 | 20724136 (11269, 11270) | Novel Protein sim. GBank g 4763871 gb AAD29655.1 AF12475 - (AF124757) aceichydroxy acid isomeroeductase [Zymomonas mobilis] | | UNCLASSIFIED | 1006 |
| 4154 | 65460060 (1823, 1824) | Novel Protein sim. GBank g 477140 pir A48751 - sperm tail protein Ms98Ca - fruit fly (Drosophila melanogaster) | | UNCLASSIFIED | 1054 |
| 4155 | 11392439 (4437, 4438) | Novel Protein sim. GBank g 4773908 gb AAD29778.1 AF14725 - (AF147259) No definition line found [Arabidopsis thaliana] | | UNCLASSIFIED | 1024 |
| 4156 | 27965558 (5467, 5468) | Novel Protein sim. GBank g 478426 pir JX0282 - sensory kinase BaS protein - Escherichia coli | | UNCLASSIFIED | 1006 |
| 4157 | 80221143 (4291, 4292) | Novel Protein sim. GBank g 479628 pir S34969 - porin E1 - Pseudomonas aeruginosa | | UNCLASSIFIED | 1024 |
| 4158 | 79181138 (16065, 16066) | Novel Protein sim. GBank g 479628 pir S34969 - porin E1 - Pseudomonas aeruginosa | | UNCLASSIFIED | 1022 |

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| 4159 | 8756873 (17654) | Novel Protein sim. GBank g 48057 pir S37051 - 4-hydroxybenzoate 3-monoxygenase (EC 1.14.13.2) - <i>Pseudomonas</i> sp | | UNCLASSIFIED | 1004 |
| 4160 | 57308551 (20083, 20084) | Novel Protein sim. GBank g 4808335 emb CAB42749.1 - (AL049841) putative membrane protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1024 |
| 4161 | 20710329 (3021, 3022) | Novel Protein sim. GBank g 4808345 emb CAB42759.1 - (AL049841) hypothetical protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1006 |
| 4162 | 20465744 (19597, 19598) | Novel Protein sim. GBank g 4808350 emb CAB42764.1 - (AL049841) possible membrane protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1010 |
| 4163 | 10872434 (14867, 14868) | Novel Protein sim. GBank g 4808397 emb CAB42729.1 - (AL049826) putative penicillin-binding protein [Streptomyces coelicolor]. | | UNCLASSIFIED | 1004 |
| 4164 | 66729137 (16609, 16610) | Novel Protein sim. GBank g 4808398 emb CAB42730.1 - (AL049826) putative transmembrane protein [Streptomyces coelicolor]. | | UNCLASSIFIED | 1049 |
| 4165 | 79264999 (10189, 10190) | Novel Protein sim. GBank g 481728 pir S39206 - hypothetical protein 1 - rat | | UNCLASSIFIED | 1007 |
| 4166 | 6749280 (9719, 9720) | Novel Protein sim. GBank g 482652 emb CAB42853.1 - (AL035402) dJ88.J8.1 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein) (hs6M1-15) [Homo sapiens] | | UNCLASSIFIED | 1022 |
| 4167 | 54680542 (1323, 1324) | Novel Protein sim. GBank g 482681 refNP_005088.1 pLGI1 - leucine-rich, glioma inactivated 1 | | UNCLASSIFIED | 1040, 1041, 1042 |
| 4168 | 55393532 (10683, 10684) | Novel Protein sim. GBank g 4826914 refNP_005081.1 pPLA2 - phospholipase A2, group IVB (cytosolic) | | UNCLASSIFIED | 1000 |

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| 4169 16178) | 30522889 (16177, Novel Protein sim. GBank gij4826934 ref NP_005125.1 pPPP4 - protein phosphatase 4, regulatory subunit 1 | | UNCLASSIFIED | 1009 |
| 4170 79177363 (13127, 13128) | Novel Protein sim. GBank gij4826998 ref NP_005057.1 pSFPQ - splicing factor proline/glutamine rich (polypyrimidine tract- binding protein-associated) | | UNCLASSIFIED | 1024 |
| 4171 20289541 (15699, 15700) | Novel Protein sim. GBank gij4836574 gb AAD30493.1 AF12644 - [AF126447] tryptophan monooxygenase [Agrobacterium vitis] | | UNCLASSIFIED | 1034 |
| 4172 20182178 (15287, 15288) | Novel Protein sim. GBank gij4836930 gb AAD30632.1 AC006008 - [AC0060085] Hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1024 |
| 4173 20480441 (5001, 5002) | Novel Protein sim. GBank gij484643 pir JQ2260 - proline-rich cell wall protein - carrot | | UNCLASSIFIED | 1022 |
| 4174 20480205 (22809, 22810) | Novel Protein sim. GBank gij484643 pir JQ2260 - proline-rich cell wall protein - carrot | | UNCLASSIFIED | 1034 |
| 4175 47656561 (17535, 17536) | Novel Protein sim. GBank gij485025 emb CAB43030.1 - (AJ239085) hypothetical protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1029, 1053 |
| 4176 54817126 (2723, 2724) | Novel Protein sim. GBank gij488342 dbj BAA05089 - (D26094) 6- aminohexanoate-dimer hydrolase [Flavobacterium sp.] | | UNCLASSIFIED | 1029 |
| 4177 79470584 (22685, 22686) | Novel Protein sim. GBank gij4883446 emb CAB43156.1 - (AL049913) hypothetical protein MLCB1610.10 [Mycobacterium leprae] | | UNCLASSIFIED | 1022 |
| 4178 95009100 (20151, 20152) | Novel Protein sim. GBank gij4884836 gb AAD31829.1 - (AF131877) NapG oxidoreductase [Streptomyces collinus] | | UNCLASSIFIED | 1017 |

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| 4179 | 78512479 (18051) (18052) | Novel Protein sim. GBank gi 4885183 ref NP_005210.1 pDIAP - diaphanous (Drosophila, homolog) 1 | | UNCLASSIFIED | 1026 |
| 4180 | 77516883 (189, 190) | Novel Protein sim. GBank gi 4887208 gb AAD32235.1 AF14744 - (AF147448) unknown [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1049 |
| 4181 | 20729752 (11095, 11096) | Novel Protein sim. GBank gi 4887209 gb AAD32236.1 AF14744 - (AF147448) lipoate biosynthesis protein B [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1006, 1010, 1022 |
| 4182 | 28842901 (20739, 20740) | Novel Protein sim. GBank gi 4887715 gb AAA79329.2 - (L08811) adherin [Drosophila melanogaster] | | UNCLASSIFIED | 1008 |
| 4183 | 78790738 (7147, 7148) | Novel Protein sim. GBank gi 4895190 gb AAD32777.1 AC00766 - (AC007661) unknown protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1026 |
| 4184 | 17876820 (15297, 15298) | Novel Protein sim. GBank gi 4902474 emb CAB43554.1 - (AJ131243) 5'- nucleotidase [Columba livia] | | UNCLASSIFIED | 1024 |
| 4185 | 70336498 (13665, 13666) | Novel Protein sim. GBank gi 4928283 gb AAD33519.1 AF13212 - (AF132127) sorbitol operon regulator [Streptococcus mutans] | | UNCLASSIFIED | 1049 |
| 4186 | 29676495 (8163, 8164) | Novel Protein sim. GBank gi 4928699 gb AAD33689.1 AF13840 - (AF136403) unknown [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1054 |
| 4187 | 10183752 (1911, 1912) | Novel Protein sim. GBank gi 496100 (L24560) - unknown function; putative [Bacteriophage phi- LC3] | | UNCLASSIFIED | 1003 |
| 4188 | 17300825 (9581, 9582) | Novel Protein sim. GBank gi 4972692 gb AAD34741.1 - (AF132153) unknown [Drosophila melanogaster] | | UNCLASSIFIED | 1008 |

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| | | | UNCLASSIFIED | 1018, 1029 |
| 4189 | 86692752 (18605, 8606) | Novel Protein sim. GBank gi 4980555 gb AAD35162.1 AE00169 - (AE001693) D-mannonate oxidoreductase, putative [Thermotoga maritima] | | |
| 4190 | 46797503 (12589, 12590) | Novel Protein sim. GBank gi 4980744 gb AAD35336.1 AE00170 - (AE001708) Na-translocating NADH-quinone reductase, Nqr2 subunit [Thermotoga maritima] | UNCLASSIFIED | 1029 |
| 4191 | 20628084 (15171, 15172) | Novel Protein sim. GBank gi 4981025 gb AAD35598.1 AE00172 - (AE001727) comM protein [Thermotoga maritima] | UNCLASSIFIED | 1010 |
| 4192 | 20627760 (8073, 8074) | Novel Protein sim. GBank gi 4981496 gb AAD36037.1 AE00175 - (AE001759) ribose ABC transporter, periplasmic ribose-binding protein [Thermotoga maritima] | UNCLASSIFIED | 1010 |
| 4193 | 37800159 (8367, 8368) | Novel Protein sim. GBank gi 4981511 gb AAD36051.1 AE00176 - (AE001760) conserved hypothetical protein, GGDEF domain [Thermotoga maritima] | UNCLASSIFIED | 1012 |
| 4194 | 20696482 (6973, 6974) | Novel Protein sim. GBank gi 4982168 gb AAD36664.1 AE00180 - (AE001804) hypothetical protein [Thermotoga maritima] | UNCLASSIFIED | 1004 |
| 4195 | 80505265 (6509, 6510) | Novel Protein sim. GBank gi 4982300 gb AAD36789.1 AE00181 - (AE001811) conserved hypothetical protein [Thermotoga maritima] | UNCLASSIFIED | 1012 |
| 4196 | 18536655 (2553, 2554) | Novel Protein sim. GBank gi 4995988 gb BAAT8221.1 - (AB021506) 25.6% identical to U1 gene of strain U1102 of HHV-6 [Human herpesvirus 6] | UNCLASSIFIED | 1017 |
| 4197 | 94723956 (9067, 9068) | Novel Protein sim. GBank gi 4996126 gb BAAT8341.1 - (AB017551) 16G2 [Homo sapiens] | UNCLASSIFIED | 1004, 1010, 1034 |

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| 4198 | 78379623 (3355, 3356) | Novel Protein sim. GBank gi 5002553 gb AAD37457.1 - (AF074603) NonF [Streptomyces griseus subsp. griseus] | | UNCLASSIFIED | 1008 |
| 4199 | 11306440 (9019, 9020) | Novel Protein sim. GBank gi 5002556 gb AAD37460.1 - (AF074603) putative flavoprotein reductase; NonH [Streptomyces griseus subsp. griseus] | | UNCLASSIFIED | 1010 |
| 4200 | 77473409 (2891, 2892) | Novel Protein sim. GBank gi 5006424 gb AAD37493.1 AF10916 - (AF109162) HmUT precursor [Corynebacterium diphtheriae] | | UNCLASSIFIED | 1023 |
| 4201 | 23291965 (2719, 2720) | Novel Protein sim. GBank gi 5019326 emb CAB44379.1 - (AL078610) putative integral membrane protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1017 |
| 4202 | 46571483 (22719, 22720) | Novel Protein sim. GBank gi 5013350 emb CAB44403.1 - (AL078610) putative heavy metal reductase [Streptomyces coelicolor] | | UNCLASSIFIED | 1029 |
| 4203 | 20478425 (6781, 6782) | Novel Protein sim. GBank gi 5031649 ref NP_005791.1 pD13S - highly charged protein | | UNCLASSIFIED | 1022 |
| 4204 | 11198755 (15589, 15590) | Novel Protein sim. GBank gi 5031657 ref NP_005755.1 pDD96 - epithelial protein up-regulated in carcinoma | | UNCLASSIFIED | 1004 |
| 4205 | 78259691 (20061, 20062) | Novel Protein sim. GBank gi 5031889 ref NP_005570.1 pLRE1 - LINE retrotransposon element 1 | | UNCLASSIFIED | 1026 |
| 4206 | 82296248 (21617, 21618) | Novel Protein sim. GBank gi 5042237 emb CAB44655.1 - (Y18605) hypothetical protein RvD1-Rv2024c' [Mycobacterium bovis BCG] | | UNCLASSIFIED | 1001, 1017, 1038 |
| 4207 | 37802702 (21535, 21536) | Novel Protein sim. GBank gi 5051775 emb CAB45068.1 - (AL078637) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1058 |

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| 4208 | 29026177 (13021, 13022) | Novel Protein sim. GBank g 5069461 gb AAD39017.1 - (AF026270) PduS [Salmonella enterica serovar Typhimurium] | | UNCLASSIFIED | 1017 |
| 4209 | 11100488 (6163, 6164) | Novel Protein sim. GBank g 5091481 gb AAD39554.1 - (AF031417) TtgC [Pseudomonas putida] | | UNCLASSIFIED | 1022 |
| 4210 | 78891509 (18777, 18778) | Novel Protein sim. GBank g 5102805 emb CAB45220.1 - (AL079308) putative membrane protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1017, 1026 |
| 4211 | 78794320 (15629, 15630) | Novel Protein sim. GBank g 5103837 gb AAD39667.1 AC00759 - (AC007591) Similar to g 43774 03 Polypeptide Deformylase from Chlamydia pneumoniae genome g AE001687. [Arabidopsis thaliana] | | UNCLASSIFIED | 1026 |
| 4212 | 38327895 (2463, 2464) | Novel Protein sim. GBank g 5103845 gb AAD39676.1 AC00759 - (AC007591) F9 1.43 [Arabidopsis thaliana] | | UNCLASSIFIED | 1008 |
| 4213 | 9849193 (13649, 13650) | Novel P'tein sim. GBank g 5104588 ldbj BAA79903.1 - (AP0000060) 254aa long hypothetical high-affinity branched-chain amino acid transport ATP-binding protein [Aeropyrum pernix] | | UNCLASSIFIED | 1008 |
| 4214 | 19867362 (10401, 10402) | Novel Protein sim. GBank g 5105618 ldbj BAA80931.1 - (AP0000062) 121aa long hypothetical protein [Aeropyrum pernix] | | UNCLASSIFIED | 1001 |
| 4215 | 65453050 (177801, 17802) | Novel Protein sim. GBank g 5107805 gb AAD25110.2 AF14055 - (AF140550) ShdA [Salmonella typhimurium] | | UNCLASSIFIED | 1049 |
| 4216 | 79951990 (18955, 18956) | Novel Protein sim. GBank g 5114184 gb AAD40230.1 AF12349 - (AF123492) Era [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1001 |
| 4217 | 17882402 (1919, 1920) | Novel Protein sim. GBank g 5123651 emb CAB45340.1 - (AL079345) putative aminotransferase [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1039 |

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| 4218 | 33202398 (7315, 7316) | Novel Protein sim. GBank g 5123878 emb CAB45470.1 - (AL079348) putative Na(+)/H(+) antiporter [Streptomyces coelicolor] | | UNCLASSIFIED | 1026 |
| 4219 | 78361326 (9315, 9316) | Novel Protein sim. GBank g 5123926 emb CAB45514.1 - (AL079350) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1003, 1044 |
| 4220 | 86474002 (14447, 14448) | Novel Protein sim. GBank g 5123944 emb CAB45502.1 - (AL079349) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1054 |
| 4221 | 78484644 (20047, 20048) | Novel Protein sim. GBank g 5139569 emb CAB45587.1 - (AL079355) putative transcriptional regulator [Streptomyces coelicolor] | | UNCLASSIFIED | 1008 |
| 4222 | 34892544 (10233, 10234) | Novel Protein sim. GBank g 5139585 emb CAB45603.1 - (AL079356) polyketide hydroxylase [Streptomyces coelicolor] | | UNCLASSIFIED | 1050 |
| 4223 | 80471534 (5325, 5326) | Novel Protein sim. GBank g 5139534 emb CAB45563.1 - (AL079353) putative penicillin-binding protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1012, 1024, 1027, 1031 |
| 4224 | 80501776 (14517, 14518) | Novel Protein sim. GBank g 515507 U12027 - Sok1p [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1003, 1004, 1009, 1012, 1022 |
| 4225 | 94991900 (3069, 3070) | Novel Protein sim. GBank g 516764 dbj BA004654 - (D21092) motor protein [Homo sapiens] | | UNCLASSIFIED | 1022 |
| 4226 | 30259581 (18109, 18110) | Novel Protein sim. GBank g 5174723 ref NP_006105.1 pTOV4 - mitochondrial outer membrane protein | | UNCLASSIFIED | 1008 |
| 4227 | 78405088 (613, 614) | Novel Protein sim. GBank g 5257110 dbj BAA81784.1 - (AB011418) orf5 [Alteromonas sp. B-10-31] | | UNCLASSIFIED | 1024 |
| 4228 | 16456835 (13059, 13060) | Novel Protein sim. GBank g 5262762 emb CAB45910.1 - (AL080283) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1008 |

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| 4229 | 79115440 (17561) | Novel Protein sim. GBank gi 5262775 emb CAB45880.1 - (AL080282) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1003 |
| 4230 | 25261625 (11719) | Novel Protein sim. GBank gi 5305335 gb AAD41594.1 AF07108 - (AF071081) proline-rich mucin homolog [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1008 |
| 4231 | 21637022 (20197) | Novel Protein sim. GBank gi 5306245 gb AAD41978.1 AC006434 - (AC006438) unknown protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1017, 1038 |
| 4232 | 29024921 (19337) | Novel Protein sim. GBank gi 532549 (U09422) - ORF16 [Enterococcus faecalis] | | UNCLASSIFIED | 1017 |
| 4233 | 30256223 (21613) | Novel Protein sim. GBank gi 5354158 gb AAD42378.1 AF14984 - (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] | | UNCLASSIFIED | 1024 |
| 4234 | 10107781 (22951) | Novel Protein sim. GBank gi 5354198 gb AAD42407.1 AF15749 - (AF157493) hypothetical protein [Zymomonas mobiliis] | | UNCLASSIFIED | 1017 |
| 4235 | 28848542 (18401) | Novel Protein sim. GBank gi 538683 pir A42800 - beta-alanine-pyruvate transaminase (EC 2.6.1.18) - Pseudomonas putida | | UNCLASSIFIED | 1026 |
| 4236 | 28477465 (14763) | Novel Protein sim. GBank gi 539030 pir B48232 - cysteine-rich extensin-like protein 2 precursor - common tobacco | | UNCLASSIFIED | 1008 |
| 4237 | 29272904 (20963) | Novel Protein sim. GBank gi 539244 pir S38100 - hypothetical protein YKR028w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 4238 | 80218605 (9611) | Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major] | | UNCLASSIFIED | 1001, 1004, 1006, 1008, 1009, 1010, 1016, 1022, 1024, 1026, 1029, 1034 |
| | 9612) | | | | |

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| 4239 | 20292803 (9911, 9912) | Novel Protein sim. GBank g 5420387 emb CAB46679.1 - (AJ243459) proteoph:sphoglycan [Leishmania major] | UNCLASSIFIED | 1034 |
| 4240 | 20451411 (16493, 16494) | Novel Protein sim. GBank g 5420387 emb CAB46679.1 - (AJ243459) proteoph:sphoglycan [Leishmania major] | UNCLASSIFIED | 1024 |
| 4241 | 70504276 (3179, 3180) | Novel Protein sim. GBank g 5420389 emb CAB46680.1 - (AJ243460) proteoph:sphoglycan [Leishmania major] | UNCLASSIFIED | 1019, 1036 |
| 4242 | 20608432 (3971, 3972) | Novel Protein sim. GBank g 5420389 emb CAB46680.1 - (AJ243460) proteoph:sphoglycan [Leishmania major] | UNCLASSIFIED | 1004 |
| 4243 | 79619222 (5367, 5368) | Novel Protein sim. GBank g 5420389 emb CAB46680.1 - (AJ243460) proteoph:sphoglycan [Leishmania major] | UNCLASSIFIED | 1038 |
| 4244 | 47660024 (17439, 17440) | Novel Protein sim. GBank g 5420319 emb CAB46680.1 - (AJ243460) proteoph:sphoglycan [Leishmania major] | UNCLASSIFIED | 1029 |
| 4245 | 70942086 (21949, 21950) | Novel Protein sim. GBank g 5430769 gb AAD43169.1 AC007550 - (AC007504) Similar to somatic embryogenesis receptor-like kinase [Arabidopsis thaliana] | UNCLASSIFIED | 1024 |
| 4246 | 19541721 (5161, 5162) | Novel Protein sim. GBank g 5434415 pir PC2022 - mucin like protein Muc2 precursor - rat (fragment) | UNCLASSIFIED | 1004 |
| 4247 | 79819430 (22981, 22982) | Novel Protein sim. GBank g 543804 sp P36670 AMPG_ECOLI - AMPG PROTEIN | UNCLASSIFIED | 1001 |
| 4248 | 79771201 (5399, 5400) | Novel Protein sim. GBank g 544119 sp Q05766 CYAA_PASMU - ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) | UNCLASSIFIED | 1034 |
| 4249 | 27844539 (3055, 3056) | Novel Protein sim. GBank g 544346 sp Q05860 FORM_MOUSE - FORMIN (IMB DEFORMITY PROTEIN) | UNCLASSIFIED | 1006 |

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| 4250 | 78154058 (11841, 11842) | Novel Protein sim. GBank gii5443461 sp Q05860 FORM_MOUSE - FORMIN (LIMB DIFFORMITY PROTEIN) | | UNCLASSIFIED | 1030, 1050 |
| 4251 | 78369003 (16773, 16774) | Novel Protein sim. GBank gii544374 sp P36417 GBF_DICDI - G-BOX BINDING FACTOR (GBF) | | UNCLASSIFIED | 1008 |
| 4252 | 20385892 (13713, 13714) | Novel Protein sim. GBank gii5457261 emb CAB46949.1 - (AL096822) putative membrane protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1004 |
| 4253 | 21426446 (20105, 20106) | Novel Protein sim. GBank gii5457287 emb CAB46974.1 - (AL096825) hypothetical protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1006 |
| 4254 | 30786324 (10973, 10974) | Novel Protein sim. GBank gii5457403 emb CAB4801.1 - (AJ238332) death inducer-2bilitator-1 [Mus musculus] | | UNCLASSIFIED | 1009 |
| 4255 | 79199218 (15631, 15632) | Novel Protein sim. GBank gii5457574 emb CAB49065.1 - (AJ248283) PAB009.1 [Pyrococcus abyssi] | | UNCLASSIFIED | 1006, 1024 |
| 4256 | 20370177 (11947, 11948) | Novel Protein sim. GBank gii5457720 emb CAB43211.1 - (AJ248283) hypothetical protein [Pyrococcus abyssi] | | UNCLASSIFIED | 1004, 1006, 1010 |
| 4257 | 27787712 (215, 216) | Novel Protein sim. GBank gii5457887 emb CAB49377.1 - (AJ248284) PAB0305 [Pyrococcus abyssi] | | UNCLASSIFIED | 1034 |
| 4258 | 10173969 (14291, 14292) | Novel Protein sim. GBank gii5458864 emb CAB53351.1 - (AJ248287) PAB237.1 [Pyrococcus abyssi] | | UNCLASSIFIED | 1023 |
| 4259 | 88094448 (4443, 4444) | Novel Protein sim. GBank gii5459219 emb CAB48892.1 - (AL096837) hypothetical protein [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1006 |
| 4260 | 86465171 (703, 704) | Novel Protein sim. GBank gii5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1029 |

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| 4261 | 20466319 (863, 864) | Novel Protein sim. G-Bank gi 5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1010 |
| 4262 | 29357646 (11391, 11392) | Novel Protein sim. G-Bank gi 5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1008 |
| 4263 | 35896045 (15247, 15248) | Novel Protein sim. G-Bank gi 545932 emb CAB50750.1 - (AL096839) conserved hypothetical protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1053 |
| 4264 | 88094861 (20165, 20166) | Novel Protein sim. G-Bank gi 545940 emb CAB50759.1 - (AL096839) putative cytochrome oxidase assembly factor [Streptomyces coelicolor] | | UNCLASSIFIED | 1004, 1010, 1022 |
| 4265 | 21129728 (19259, 19260) | Novel Protein sim. G-Bank gi 547153 sp P35915 HMGCL_CHICK- HYDROXYMETHYLGLUTARYL-COA LYASE (HMG-COA LYASE) (HL) (3-HYDROXY-3-METHYLGLUTARATE-COA LYASE) | | UNCLASSIFIED | 1034 |
| 4266 | 25267091 (13835, 13836) | Novel Protein sim. G-Bank gi 5478797 dbj BAI82479.1 - (AB021310) chlorophyll b synthase [Oryza sativa] | | UNCLASSIFIED | 1023 |
| 4267 | 65661339 (17341, 17342) | Novel Protein sim. G-Bank gi 548564 sp P36304 POLR_KYMVJ - RNA REPLICASE POLYPROTEIN | | UNCLASSIFIED | 1016 |
| 4268 | 78761774 (13415, 13416) | Novel Protein sim. G-Bank gi 548562 sp P10963 PPCK_YEAST - PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) | | UNCLASSIFIED | 1044 |
| 4269 | 80409035 (6347, 6348) | Novel Protein sim. G-Bank gi 548705 sp P36949 RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR | | UNCLASSIFIED | 1029 |

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| 4270 | 8523867 (18799, 18800) | Novel Protein sim. GBank g 548925 sp P36024 SIS2_YEAST - SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3) | UNCLASSIFIED | 1022 |
| 4271 | 65894777 (11929, 11930) | Novel Protein sim. GBank g 549613 sp P36136 YK23_YEAST - HYPOTHETICAL 31.0 KD PROTEIN IN GAP1- NAP1 INTERGENIC REGION | UNCLASSIFIED | 1016, 1023 |
| 4272 | 28486888 (5997, 5998) | Novel Protein sim. GBank g 549624 sp P36146 LAS1_YEAST - LAS1 PROTEIN | UNCLASSIFIED | 1026 |
| 4273 | 85513339 (15099, 15100) | Novel Protein sim. GBank g 549634 sp P36156 YK56_YEAST - HYPOTHETICAL 43.3 KD PROTEIN IN SIS2- MTD1 INTERGENIC REGION | UNCLASSIFIED | 1001, 1003, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1025, 1026, 1027, 1031, 1034, 1038, 1039, 1044, 1049 |
| 4274 | 29261145 (11205, 11206) | Novel Protein sim. GBank g 549636 sp P36158 YK58_YEAST - HYPOTHETICAL 68.3 KD PROTEIN IN SIS2- MTD1 INTERGENIC REGION | UNCLASSIFIED | 1009 |
| 4275 | 25341189 (7617, 7618) | Novel Protein sim. GBank g 549643 sp P36165 YK69_YEAST - HYPOTHETICAL 102.7 KD PROTEIN IN PRP16- SRP40 INTERGENIC REGION | UNCLASSIFIED | 1044 |
| 4276 | 78461719 (13971, 13972) | Novel Protein sim. GBank g 549643 sp P36165 YK69_YEAST - HYPOTHETICAL 102.7 KD PROTEIN IN PRP16- SRP40 INTERGENIC REGION | UNCLASSIFIED | 1008 |
| 4277 | 80027280 (6545, 6546) | Novel Protein sim. GBank g 549704 sp P36075 YK10_YEAST - HYPOTHETICAL 50.9 KD PROTEIN IN BUD2- MIF2 INTERGENIC REGION | UNCLASSIFIED | 1001, 1004, 1006 |

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| 4278 | 20484209 (13947, 13948) | Novel Protein sim. GBank g 549734 sp P36051 YKQ5_YEAST - HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION | | UNCLASSIFIED | 1008, 1009, |
| 4279 | 80217125 (6487, 6488) | Novel Protein sim. GBank g 549767 sp P36111 YK25_YEAST - HYPOTHETICAL 66.6 KD PROTEIN IN YPT52-DBP7 INTERGENIC REGION | | UNCLASSIFIED | 1022, 1024, 1029 |
| 4280 | 79615128 (7139, 7140) | Novel Protein sim. GBank g 549814 sp Q01856 YRDX_RHOSH - HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN RDXA 3 REGION | | UNCLASSIFIED | 1003 |
| 4281 | 78245861 (3899, 3900) | Novel Protein sim. GBank g 549854 (U07615) - mucin [Rattus norvegicus] | | UNCLASSIFIED | 1006 |
| 4282 | 32275610 (579, 580) | Novel Protein sim. GBank g 551477 emb CAB50780.1 - (X74216) TdA protein [Pseudomonas putida] | | UNCLASSIFIED | 1029 |
| 4283 | 25263625 (3835, 3836) | Novel Protein sim. GBank g 551478 emb CAB50783.1 - (X74218) hypothetical protein [Pseudomonas putida] | | UNCLASSIFIED | 1026 |
| 4284 | 37797702 (12461, 12462) | Novel Protein sim. GBank g 552506 emb CAB50880.1 - (AL096844) putative integral membrane transporter [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1012 |
| 4285 | 80502199 (12497, 12498) | Novel Protein sim. GBank g 553136 emb CAB50998.1 - (AL096852) hypothetical protein [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1003, 1008, 1010, 1012, 1024 |
| 4286 | 86471967 (9293, 9294) | Novel Protein sim. GBank g 553190 gb AAD44524.1 AF10740 - (AF107406) GW128 [Homo sapiens] | | UNCLASSIFIED | 1029 |
| 4287 | 80227840 (13667, 13668) | Novel Protein sim. GBank g 554015 (M37679) - Ig heavy chain precursor [Mus musculus] | | UNCLASSIFIED | 1006 |
| 4288 | 47657338 (1277, 1278) | Novel Protein sim. GBank g 556614 (U14909) - MtrB [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1029 |

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| 4289 | 80503062 (15163, 15164) | Novel Protein sim. GBank g 5578872 emb CAB51274.1 - (AL096872) hypothetical protein [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1004, 1006, 1012, 1017, 1024, 1034 |
| 4290 | 80248867 (16467, 16468) | Novel Protein sim. GBank g 5578875 emb CAB51277.1 - (AL096872) putative lipote-protein ligase [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1006, 1053 |
| 4291 | 79319416 (2413, 2414) | Novel Protein sim. GBank g 5579421 gb AAD45542.1 U70376_- (U70376) Orf2 [Streptomyces flavopersicus] | | UNCLASSIFIED | 1022 |
| 4292 | 27977871 (1525, 1526) | Novel Protein sim. GBank g 5566803 emb CAB51450.1 - (AL096884) putative transcriptional regulatory protein [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1006 |
| 4293 | 27366056 (9249, 9250) | Novel Protein sim. GBank g 5613074 gb AAD45616.1 AF06194 - (AF061943) protease-derived STE20-like kinase PSK [Homo sapiens] | | UNCLASSIFIED | 1022 |
| 4294 | 24144612 (15437, 15438) | Novel Protein sim. GBank g 5640135 emb CAA64209.1 - (X94435) ribosomal protein TL5 [Thermus thermophilus] | | UNCLASSIFIED | 1001, 1003 |
| 4295 | 27956694 (22021, 22022) | Novel Protein sim. GBank g 5668580 gb AAD45664.1 AF05115 - (AF051150) aspartyl protease [Mus musculus] | | UNCLASSIFIED | 1004, 1022 |
| 4296 | 28474907 (20215, 20216) | Novel Protein sim. GBank g 5668806 gb AAD46032.1 AC00751 - (AC007519) Strong similarity to F16N3.17 from Arabidopsis thaliana BAC gb AC007519. [Arabidopsis thaliana] | | UNCLASSIFIED | 1026 |
| 4297 | 94631802 (4247, 4248) | Novel Protein sim. GBank g 5688851 dbj BAA82702.1 - (AB017438) Orf5 [Streptomyces coelicolor] | | UNCLASSIFIED | 1006, 1031 |
| 4298 | 10083399 (1191, 1192) | Novel Protein sim. GBank g 5689395 dbj BAA82981.1 - (AB028952) KIAA1029 protein [Homo sapiens] | | UNCLASSIFIED | 1044 |

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| 4289 | 78936219 (17531) | Novel Protein sim. GBank gi 5689465 emb BAA83016.1 - (AB028987) KIAA1061 protein [Homo sapiens] | UNCLASSIFIED | 1044, 1050 |
| 4300 | 13088718 (18587) (18588) | Novel Protein sim. GBank gi 5689491 emb BAA83029.1 - (AB029000) KIAA107' protein [Homo sapiens] | UNCLASSIFIED | 1027 |
| 4301 | 24121020 (10605) (10606) | Novel Protein sim. GBank gi 5689513 emb BAA83040.1 - (AB029011) KIAA1088 protein [Homo sapiens] | UNCLASSIFIED | 1029 |
| 4302 | 88095253 (17405) (17406) | Novel Protein sim. GBank gi 5689525 emb BAA83046.1 - (AB029017) KIAA1094 protein [Homo sapiens] | UNCLASSIFIED | 1034 |
| 4303 | 30660456 (4139, 4140) | Novel Protein sim. GBank gi 5689551 emb BAA83059.1 - (AB029030) KIAA110' protein [Homo sapiens] | UNCLASSIFIED | 1026 |
| 4304 | 30660312 (9653, 9654) | Novel Protein sim. GBank gi 5689571 emb BAA83059.1 - (AB029030) KIAA110' protein [Homo sapiens] | UNCLASSIFIED | 1026 |
| 4305 | 78459851 (8605, 8606) | Novel Protein sim. GBank gi 5689883 emb CAB52046.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)] | UNCLASSIFIED | 1023, 1026, 1029, 1053 |
| 4306 | 20286969 (17575, 17576) | Novel Protein sim. GBank gi 5689958 emb CAB51995.1 - (AL109663) putative UDP-N-acetylglucosaminidase | UNCLASSIFIED | 1004, 1006, 1025, 1034 |
| 4307 | 79822009 (16001, 16002) | Novel Protein sim. GBank gi 5689961 emb CAB51998.1 - (AL109663) putative UDP-N-acetylglucosaminidase | UNCLASSIFIED | 1034 |
| 4308 | 79631297 (8077, 8078) | Novel Protein sim. GBank gi 5689967 emb CAB52004.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)] | UNCLASSIFIED | 1008, 1023, 1027 |

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| 4309 | 11085397 (19439, 19440) | Novel Protein sim. GBank g!5690013!emb CAB51940.11 - (AJ132472) Putative ABC-type Sugar Transporter [Ruminococcus flavefaciens] | | UNCLASSIFIED | 1024 |
| 4310 | 13418034 (21103, 21104) | Novel Protein sim. GBank g!5708250!emb CAB52363.11 - (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)] | | UNCLASSIFIED | 1022 |
| 4311 | 11817576 (17589, 17590) | Novel Protein sim. GBank g!584706!sp P37833 ATC_ORYSA- ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSMINASE A) | | UNCLASSIFIED | 1004 |
| 4312 | 78895482 (22707, 22708) | Novel Protein sim. GBank g!585369!sp P38620 KPR2_YEAST - RIBOSE- PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 2) | | UNCLASSIFIED | 1039 |
| 4313 | 11611991 (7747, 7748) | Novel Protein sim. GBank g!585377!sp P38131 KTR4_YEAST - PROBABLE MANNOSYLTRANSFERASE KTR4 | | UNCLASSIFIED | 1006 |
| 4314 | 80237342 (17327, 17328) | Novel Protein sim. GBank g!585465!sp P29469 MCM2_YEAST - MINICHROMOSOME MAINTENANCE PROTEIN 2 | | UNCLASSIFIED | 1006, 1008, 1009, 1022, 1034 |
| 4315 | 13523408 (21665, 21666) | Novel Protein sim. GBank g!585774!sp P24386 RAE1_HUMAN - RAB PROTEINS GERANYLGERANYLTRANSFERASE COMPONENT A 1 (RAB ESCORT PROTEIN 1) (REP-1) (CHOROIDERAEMIA PROTEIN) (TCD PROTEIN) | | UNCLASSIFIED | 1024 |
| 4316 | 79763698 (14811, 14812) | Novel Protein sim. GBank g!586056!sp P00961 SYGB_ECOLI - GLYCYL- TRNA SYNTHETASE BETA CHAIN (GLYCINE- TRNA LIGASE BETA CHAIN) (GLYRS) | | UNCLASSIFIED | 1003 |

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| 4325 | 11359873 (18683, 18694) | Novel Protein sim. GBank gi 5864961 sp P38235 YBQ3_YEAST - HYPOTHETICAL 40.3 KD PROTEIN IN REG2- YRQ2 INTERGENIC REGION | | UNCLASSIFIED | 1006 |
| 4326 | 78792061 (5865, 5866) | Novel Protein sim. GBank gi 5865041 sp P382411 YBR5_YEAST - HYPOTHETICAL 40.9 KD PROTEIN IN ORC2- TIP1 INTERGENIC REGION | | UNCLASSIFIED | 1009 |
| 4327 | 80248150 (16183, 16184) | Novel Protein sim. GBank gi 5865171 sp P38250 YBT6_YEAST - HYPOTHETICAL 105.9 KD PROTEIN IN AAC3- RFC5 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1006, 1009, 1031, 1034, 1039 |
| 4328 | 79439310 (10891, 10892) | Novel Protein sim. GBank gi 5865281 sp P38261 YBV2_YEAST - HYPOTHETICAL 85.5 KD PROTEIN IN VPS15- YMC2 INTERGENIC REGION | | UNCLASSIFIED | 1034 |
| 4329 | 18598518 (11171, 11172) | Novel Protein sim. GBank gi 5865330 sp P38263 YBV5_YEAST - HYPOTHETICAL 41.2 KD PROTEIN IN YMC2- CMD1 INTERGENIC REGION | | UNCLASSIFIED | 1023 |
| 4330 | 28782605 (4771, 4772) | Novel Protein sim. GBank gi 5865331 sp P38266 YBV8_YEAST - HYPOTHETICAL 92.8 KD PROTEIN IN YMC2- CMD1 INTERGENIC REGION | | UNCLASSIFIED | 1026 |
| 4331 | 19887696 (14247, 14248) | Novel Protein sim. GBank gi 586870 sp P37540 HOI_B_BACSU - DNA POLYMERASE III, DELTA' SUBUNIT | | UNCLASSIFIED | 1034 |
| 4332 | 79205017 (2773, 2774) | Novel Protein sim. GBank gi 586876 sp P37546 YABE_BACSU - HYPOTHETICAL 47.7 KD PROTEIN IN METS- KSGA INTERGENIC REGION | | UNCLASSIFIED | 1054 |
| 4333 | 27981381 (3129, 3130) | Novel Protein sim. GBank gi 586877 sp P37547 YABF_BACSU - HYPOTHETICAL 20.7 KD PROTEIN IN METS- KSGA INTERGENIC REGION | | UNCLASSIFIED | 1006 |

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| 4334 | 80052555 (19417, 19418) | Novel Protein sim. GBank gil625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae] | UNCLASSIFIED | 1010 |
| 4335 | 39723336 (13767, 13768) | Novel Protein sim. GBank gil625184 (L36957) - mitochondrial isoleucyl-tRNA synthetase [Saccharomyces cerevisiae] | UNCLASSIFIED | 1050 |
| 4336 | 33183575 (5793, 5794) | Novel Protein sim. GBank gil626375 pir S48472 - probable membrane protein YIL100c-a - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1026 |
| 4337 | 27962609 (14557, 14558) | Novel Protein sim. GBank gil626441 pir S48569 - hypothetical protein YLR219w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1034 |
| 4338 | 39402485 (5407, 5408) | Novel Protein sim. GBank gil626642 pir S46723 - arginine-tRNA ligase (EC 6.1.1.19), mitochondrial -yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1004, 1006, 1016, 1022, 1024 |
| 4339 | 79858563 (14529, 14530) | Novel Protein sim. GBank gil628110 pir S32975 - hypothetical protein - human herpesvirus 4 | UNCLASSIFIED | 1023 |
| 4340 | 39564742 (7519, 7520) | Novel Protein sim. GBank gil628710 pir S41739 - hypothetical protein - Escherichia coli | UNCLASSIFIED | 1004 |
| 4341 | 10218925 (7227, 7228) | Novel Protein sim. GBank gil630472 pir A54138 - acidic repetitive protein arp1 - Tetrahymena thermophila (SGC5) | UNCLASSIFIED | 1039 |
| 4342 | 94675524 (2759, 2760) | Novel Protein sim. GBank gil664571 pir XYPST7A - site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) PaerT1 - Pseudomonas aeruginosa plasmid pMG7 | UNCLASSIFIED | 1022 |
| 4343 | 388922016 (1179, 1180) | Novel Protein sim. GBank gil683778 emb CAA88374 - (Z48483) unknown [Saccharomyces cerevisiae] | UNCLASSIFIED | 1008 |
| 4344 | 78043821 (2275, 2276) | Novel Protein sim. GBank gil68563 pir YFBSS - phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Bacillus subtilis | UNCLASSIFIED | 1054 |

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| 4345 | 19872489 (17983, 17984) | Novel Protein sim. GBank gi 68663 pir YFBSB - phenylalanine--tRNA ligase (EC 6.1.1.20) beta Chain . <i>Bacillus subtilis</i> | UNCLASSIFIED | 1034 |
| 4346 | 80423236 (18755, 18756) | Novel Protein sim. GBank gi 688011bbs 15930 - (S73498) AgX-1 antigen [human, infertile patient, testis, Peptide, 505 aa] [Homo sapiens] | UNCLASSIFIED | 1008, 1023, 1024, 1025, 1039, 1044 |
| 4347 | 29243304 (1507, 1508) | Novel Protein sim. GBank gi 699144 (U15180) - DNA-3-methyladenine glycosidase I [Mycobacterium leprae] | UNCLASSIFIED | 1026 |
| 4348 | 47661876 (18273, 18274) | Novel Protein sim. GBank gi 699161 (U15181) - hypothetical protein [Mycobacterium leprae] | UNCLASSIFIED | 1029 |
| 4349 | 78475388 (7823, 7824) | Novel Protein sim. GBank gi 727399 gb AAB66588 - (U22837) HmSH [Yersinia pestis] | UNCLASSIFIED | 1003 |
| 4350 | 30407690 (11585, 11586) | Novel Protein sim. GBank gi 728659 emb CAA88527 - (Z48613) unknown [Saccharomyces cerevisiae] | UNCLASSIFIED | 1008 |
| 4351 | 78674094 (3323, 3324) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1026 |
| 4352 | 86671150 (4579, 4580) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1007, 1019 |
| 4353 | 87128324 (5383, 5384) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1025, 1026 |
| 4354 | 17958326 (7329, 7330) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1016 |
| 4355 | 16375635 (7945, 7946) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1054 |
| 4356 | 91231298 (8513, 8514) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1010 |

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| 4357 | 86668127 (9723, 9724) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1008, 1029 |
| 4358 | 49320730 (11981, 11982) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1040 |
| 4359 | 91226056 (12073, 12074) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1010 |
| 4360 | 10141581 (12539, 12540) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1025 |
| 4361 | 54531534 (12605, 12606) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1041 |
| 4362 | 78486472 (13833, 13834) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1026 |
| 4363 | 78890237 (15625, 15626) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1024 |
| 4364 | 37016371 (16081, 16082) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1025 |
| 4365 | 79775055 (18705, 18706) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1003, 1023, 1044 |
| 4366 | 13520123 (20591, 20592) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1024 |
| 4367 | 90935104 (20959, 20960) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1020 |
| 4368 | 54536980 (21533, 21534) | Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!! | UNCLASSIFIED | 1041 |

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| 4369 | 66525975 (22005, 22006) | Novel Protein sim. GBank g 728831 sp P39198 ALU1_HUMAN - !!!! ALU SUBFAMILY J WARNING ENTRY !!!! | UNCLASSIFIED | 1022, 1038, 1054 |
| 4370 | 10128936 (6717, 6718) | Novel Protein sim. GBank g 728832 sp P39189 ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! | UNCLASSIFIED | 1025 |
| 4371 | 78675523 (16479, 16480) | Novel Protein sim. GBank g 728832 sp P39189 ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! | UNCLASSIFIED | 1026 |
| 4372 | 77918603 (20741, 20742) | Novel Protein sim. GBank g 728832 sp P39189 ALU2_HUMAN - !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! | UNCLASSIFIED | 1019, 1036 |
| 4373 | 79844234 (7229, 7230) | Novel Protein sim. GBank g 728835 sp P39192 ALU5_HUMAN - !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! | UNCLASSIFIED | 1044 |
| 4374 | 71329591 (13295, 13296) | Novel Protein sim. GBank g 728836 sp P39193 ALU6_HUMAN - !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! | UNCLASSIFIED | 1026, 1050 |
| 4375 | 78282764 (8865, 8866) | Novel Protein sim. GBank g 728837 sp P39194 ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! | UNCLASSIFIED | 1029 |
| 4376 | 46691574 (17919, 17920) | Novel Protein sim. GBank g 728837 sp P39194 ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! | UNCLASSIFIED | 1065 |
| 4377 | 18403567 (20451, 20452) | Novel Protein sim. GBank g 728837 sp P39194 ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! | UNCLASSIFIED | 1004 |
| 4378 | 27369084 (21417, 21418) | Novel Protein sim. GBank g 728837 sp P39194 ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! | UNCLASSIFIED | 1026 |
| 4379 | 79556315 (4777, 4778) | Novel Protein sim. GBank g 728838 sp P39195 ALU8_HUMAN - !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! | UNCLASSIFIED | 1023 |

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| 4380 | 95199241 (16767, 16768) | Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) | UNCLASSIFIED | 1027, 1029 |
| 4381 | 78776077 (16277, 16278) | Novel Protein sim. GBank gi 728868 sp P40603 APG_BRANA - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) | UNCLASSIFIED | 1009, 1017 |
| 4382 | 78908326 (18211, 18212) | Novel Protein sim. GBank gi 728868 sp P40603 APG_BRANA - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) | UNCLASSIFIED | 1044 |
| 4383 | 82062189 (6407, 6408) | Novel Protein sim. GBank gi 729352 sp P32354 DN43_YEAST - DNA43 PROTEIN | UNCLASSIFIED | 1003, 1004, 1006, 1010, 1012, 1016, 1022, 1023, 1024, 1029, 1034, 1038 |
| 4384 | 80464569 (381, 382) | Novel Protein sim. GBank gi 729534 sp P21373 UTR1_YEAST - UTR1 PROTEIN (UNKNOWN TRANSCRIPT 1 PROTEIN) | UNCLASSIFIED | 1008, 1010, 1012, 1017, 1022, 1023, 1030, 1034, 1038, 1039, 1044 |
| 4385 | 20702426 (22225, 22226) | Novel Protein sim. GBank gi 729721 sp P07172 HIS8_YEAST - HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (IMIDAZOLE ACETOL-PHOSPHATE TRANSAMINASE) | UNCLASSIFIED | 1022 |
| 4386 | 20438387 (701, 702) | Novel Protein sim. GBank gi 729747 sp P39662 HMPA_ALCEU - FLAVOHEMOPOROTEIN (HAEMOGLOBIN-LIKE PROTEIN) (FLAVOHEMOGLOBIN) | UNCLASSIFIED | 1010 |
| 4387 | 78747957 (4401, 4402) | Novel Protein sim. GBank gi 730197 sp P40354 INTA1_YEAST - PROTEIN N TERMINAL AMIDASE (NT-AMIDASE) | UNCLASSIFIED | 1044 |

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| 4388 | 38922472 (20645, 20646) | Novel Protein sim. GBank PROTEIN gi 730779 sp P38904 SP41_YEAST - SPP41 | | UNCLASSIFIED | 1008 |
| 4389 | 79853762 (15439, 15440) | Novel Protein sim. GBank gi 730887 sp P08956 T1R_ECOLI - TYPE I RESTRICTION ENZYME ECOK1 R PROTEIN | | UNCLASSIFIED | 1044 |
| 4390 | 71760881 (275, 276) | Novel Protein sim. GBank gi 730888 sp Q06666 T12_MOUSE - OCTAPEPTIDE-REPEAT PROTEIN T2 | | UNCLASSIFIED | 1008 |
| 4391 | 78460840 (12843, 12844) | Novel Protein sim. GBank gi 730986 sp P41068 TRAP_ECOLI - TRAP PROTEIN | | UNCLASSIFIED | 1044 |
| 4392 | 27974366 (16869, 16870) | Novel Protein sim. GBank gi 731010 sp Q00188 TRL4_ECOLI - TRAL PROTEIN | | UNCLASSIFIED | 1022 |
| 4393 | 71844493 (9191, 9192) | Novel Protein sim. GBank gi 731301 sp P27637 YA14_YEAST - HYPOTHETICAL 78.3 KD PROTEIN IN SEN34- ADE1 INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 4394 | 29242614 (20073, 20074) | Novel Protein sim. GBank gi 731367 sp P38962 YD66_YEAST - HYPOTHETICAL 23.1 KD PROTEIN IN STN1- AFR1 INTERGENIC REGION | | UNCLASSIFIED | 1017 |
| 4395 | 30263127 (6229, 6230) | Novel Protein sim. GBank gi 731404 sp P39996 YE87_YEAST - HYPOTHETICAL 38.2 KD PROTEIN IN PMP2- VAC8 INTERGENIC REGION | | UNCLASSIFIED | 1008 |
| 4396 | 10166025 (11565, 11566) | Novel Protein sim. GBank gi 731434 sp P40008 YEJ4_YEAST - HYPOTHETICAL 25.1 KD PROTEIN IN PMI40- PAC2 INTERGENIC REGION | | UNCLASSIFIED | 1024 |
| 4397 | 79611412 (10225, 10226) | Novel Protein sim. GBank gi 731524 sp P40090 YEX7_YEAST - HYPOTHETICAL 72.1 KD PROTEIN IN FTR1- SPT15 INTERGENIC REGION | | UNCLASSIFIED | 1008 |

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| 4398 | 30604031 (1381, 1382) | Novel Protein sim. GBank g I 731525 sp P40091 PEA2_YEAST - PEA2 PROTEIN(N (PPF2 PROTEIN) | | UNCLASSIFIED | 1022 |
| 4399 | 27926460 (20727, 20728) | Novel Protein sim. GBank g I 731530 sp P40095 YEY8_YEAST - HYPOTHETICAL 63.7 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 4400 | 71845439 (4597, 4598) | Novel Protein sim. GBank g I 731580 sp P38894 FL05_YEAST - FLOCCULATION PROTEIN FL05 PRECURSOR (FL0CCULIN 5) | | UNCLASSIFIED | 1022 |
| 4401 | 29264714 (20439, 20440) | Novel Protein sim. GBank g I 731604 sp P38742 YHC3_YEAST - HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1004, 1006, 1022, 1024, 1034 |
| 4402 | 82457087 (12377, 12378) | Novel Protein sim. GBank g I 731672 sp P38793 YHNO_YEAST - HYPOTHETICAL 56.5 KD PROTEIN IN DYS1-ERG7 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1024, 1026, 1031, 1034, 1039, 1044, 1050 |
| 4403 | 11354327 (9927, 9928) | Novel Protein sim. GBank g I 731678 sp P38799 YHN8_YEAST - HYPOTHETICAL 63.3 KD PROTEIN IN NMD2-IRE1 INTERGENIC REGION | | UNCLASSIFIED | 1058 |
| 4404 | 80250819 (5231, 5232) | Novel Protein sim. GBank g I 731680 sp P38801 YHO1_YEAST - HYPOTHETICAL 21.0 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1006, 1012, 1022, 1024, 1027, 1038, 1044 |
| 4405 | 56117620 (17131, 17132) | Novel Protein sim. GBank g I 731726 sp P32900 YHU9_YEAST - HYPOTHETICAL 81.8 KD PROTEIN IN MRPL6-SPO12 INTERGENIC REGION | | UNCLASSIFIED | 1008, 1030 |

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| 4406 | 80430434 (4527, 4528) | Novel Protein sim. GBank g I731727 sp P38848 YHV0_YEAST - HYPOTHETICAL 66.1 KD PROTEIN IN MRPL6-SPO12 INTERGENIC REGION | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1016, 1022, 1024, 1025, 1031, 1034, 1038, 1039, 1040, 1054 |
| 4407 | 29684180 (14571, 14572) | Novel Protein sim. GBank g I731737 sp P38858 SOL3_YEAST - SOL3 PROTEIN | UNCLASSIFIED | 1009 |
| 4408 | 34114340 (7241, 7242) | Novel Protein sim. GBank g I731739 sp P38860 YHW8_YEAST - HYPOTHETICAL 55.5 KD GTP BINDING PROTEIN IN CDC23-DBP8 INTERGENIC REGION | UNCLASSIFIED | 1000 |
| 4409 | 78729008 (17649, 17650) | Novel Protein sim. GBank g I731757 sp P38874 IK1_YEAST - IK1 PROTEIN | UNCLASSIFIED | 1008 |
| 4410 | 57292768 (4403, 4404) | Novel Protein sim. GBank g I731758 sp P38875 YHY8_YEAST - HYPOTHETICAL 67.8 KD PROTEIN IN IK1-ERG9 INTERGENIC REGION | UNCLASSIFIED | 1001, 1009, 1022, 1024, 1026 |
| 4411 | 21418073 (17393, 17394) | Novel Protein sim. GBank g I731779 sp P40552 YB1_YEAST - HYPOTHETICAL 26.3 KD PROTEIN IN PDR11-FAA3 INTERGENIC REGION | UNCLASSIFIED | 1004 |
| 4412 | 20732337 (19551, 19552) | Novel Protein sim. GBank g I731805 sp P40528 SYG1_YEAST - SYG1 PROTEIN | UNCLASSIFIED | 1010 |
| 4413 | 27849057 (16197, 16198) | Novel Protein sim. GBank g I731813 sp P40523 YIF5_YEAST - HYPOTHETICAL 70.7 KD PROTEIN IN SNP1-GPP1 INTERGENIC REGION | UNCLASSIFIED | 1022, 1034 |

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| 4414 | 17123843 (22029) 22030) | Novel Protein sim. GBank gi 731813 sp P40523 YIF5_YEAST - HYPOTHETICAL 70.7 KD PROTEIN IN SNP1- GPP1 IN TERGENIC REGION | UNCLASSIFIED | 1017 |
| 4415 | 78770255 (22693) 22694) | Novel Protein sim. GBank gi 731818 sp P40188 YF7_YEAST - HYPOTHETICAL 19.2 KD PROTEIN IN SNP1- GPP1 IN TERGENIC REGION | UNCLASSIFIED | 1003, 1008, 1009, 1022 |
| 4416 | 95293324 (18567, 18568) | Novel Protein sim. GBank gi 731821 sp P40517 YG3_YEAST - HYPOTHETICAL 36.1 KD PROTEIN IN RNR3- ARC15 INTERGENIC REGION | UNCLASSIFIED | 1004, 1022, 1024 |
| 4417 | 71808933 (14585, 14586) | Novel Protein sim. GBank gi 731842 sp P40498 YU1_YEAST - HYPOTHETICAL 84.0 KD PROTEIN IN SGA1- KTR7 INTERGENIC REGION | UNCLASSIFIED | 1008, 1022 |
| 4418 | 78910859 (9217, 9218) | Novel Protein sim. GBank gi 73185 sp P40489 YK1_YEAST - HYPOTHETICAL 72.7 KD PROTEIN IN MOB1- SGA1 IN TERGENIC REGION | UNCLASSIFIED | 1003 |
| 4419 | 78911074 (21719, 21720) | Novel Protein sim. GBank gi 731853 sp P40486 YK4_YEAST - HYPOTHETICAL 59.2 KD PROTEIN IN MOB1- SGA1 IN TERGENIC REGION | UNCLASSIFIED | 1003, 1008 |
| 4420 | 25146202 (20849, 20850) | Novel Protein sim. GBank gi 731862 sp P40477 N159_YEAST - NUCLEOPORIN NUP159 (NUCLEAR PORE PROTEIN NUP159) | UNCLASSIFIED | 1026 |
| 4421 | 80078055 (11065, 11066) | Novel Protein sim. GBank gi 731864 sp P40475 YMO_YEAST - HYPOTHETICAL 61.8 KD PROTEIN IN KGD1- SIM1 INTERGENIC REGION | UNCLASSIFIED | 1017, 1022, 1034 |
| 4422 | 79556341 (2895, 2896) | Novel Protein sim. GBank gi 731871 sp P40468 YIM9_YEAST - HYPOTHETICAL 269.9 KD PROTEIN IN FKH1- MET18 INTERGENIC REGION | UNCLASSIFIED | 1025 |

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| 4423 | 19883506 (14844) | Novel Protein sim. GBank gi 731904 sp P4056 YIS1_YEAST - HYPOTHETICAL 29.0 KD PROTEIN IN BET1- PAN1 INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 4424 | 80219116 (6983, 6984) | Novel Protein sim. GBank gi 731935 sp P40362 YJG9_YEAST - HYPOTHETICAL 66.4 KD PROTEIN IN SMC3- MRPL8 INTERGENIC REGION | | UNCLASSIFIED | 1006, 1009, 1010, 1022, 1024, 1034, 1039 |
| 4425 | 78675785 (4325, 4326) | Novel Protein sim. GBank gi 731940 sp P40367 YJG2_YEAST - HYPOTHETICAL 94.9 KD PROTEIN IN MRPL8- NUP82 INTERGENIC REGION | | UNCLASSIFIED | 1017 |
| 4426 | 79374109 (18553, 18554) | Novel Protein sim. GBank gi 731940 sp P40367 YJG2_YEAST - HYPOTHETICAL 94.9 KD PROTEIN IN MRPL8- NUP82 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1022 |
| 4427 | 28806620 (719, 720) | Novel Protein sim. GBank gi 731942 sp P39526 YJU7_YEAST - HYPOTHETICAL 229.9 KD PROTEIN IN NUC1- NCE1 INTERGENIC REGION | | UNCLASSIFIED | 1004, 1022 |
| 4428 | 79588597 (22955, 22956) | Novel Protein sim. GBank gi 731971 sp P40856 S185_YEAST - SIT4- ASSOCIATING PROTEIN SAP185 | | UNCLASSIFIED | 1022, 1026 |
| 4429 | 80059406 (7689, 7690) | Novel Protein sim. GBank gi 732097 sp P39389 YJIR_ECOLI - HYPOTHETICAL 53.0 KD PROTEIN IN IADA- MCRD INTERGENIC REGION (F470) | | UNCLASSIFIED | 1024, 1026 |
| 4430 | 79567067 (11507, 11508) | Novel Protein sim. GBank gi 732104 sp P39396 YJY_ECOLI - HYPOTHETICAL 77.9 KD PROTEIN IN MRR- TSR INTERGENIC REGION (F721) | | UNCLASSIFIED | 1044 |
| 4431 | 80249668 (10519, 10520) | Novel Protein sim. GBank gi 732167 sp P40219 M25_YEAST - HYPOTHETICAL 16.4 KD PROTEIN IN TIF34- SWP1 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1022, 1024 |

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| 4432 | 14895374 (14775) | Novel Protein sim. GBank gil 732344 sp P39597 YWBN_BACSU - HYPOTHETICAL 45.7 KD PROTEIN IN EPR-GALK INTERGENIC REGION PRECURSOR | | |
| 4433 | 24115247 (11387) | Novel Protein sim. GBank gil 740613 pfr 2005409A - rhodopsin [Alloteuthis subulata] | UNCLASSIFIED | 1029 |
| 4434 | 80082341 (20837) | Novel Protein sim. GBank gil 746474 U23511 - weakly similar to dihydrokaempferol 4-reductase [Caenorhabditis elegans] | UNCLASSIFIED | 1034 |
| 4435 | 20292082 (4133, 4134) | Novel Protein sim. GBank gil 757830 emb CAA86044 - (Z37980) 2-oxo-hept-3-ene-1,7-dioate hydratase [Escherichia coli] | UNCLASSIFIED | 1024, 1034 |
| 4436 | 21425934 (7391, 7392) | Novel Protein sim. GBank gil 758210 emb CAA55681 - (X79076) 2-halobenzoate 1,2-dioxygenase [Burkholderia cepacia] | UNCLASSIFIED | 1022 |
| 4437 | 78766703 (13061, 13062) | Novel Protein sim. GBank gil 767189 pir Q3ECBA - hypothetical 17K protein (bioA '3' region) - Escherichia coli | UNCLASSIFIED | 1026 |
| 4438 | 79630475 (4837, 4838) | Novel Protein sim. GBank gil 76204 pir QQECW7 - hypothetical protein 76 - Escherichia coli | UNCLASSIFIED | 1039 |
| 4439 | 78769985 (22183, 22184) | Novel Protein sim. GBank gil 763391 emb CAA52881 - (X74920) SNG1 [Saccharomyces cerevisiae] | UNCLASSIFIED | 1026 |
| 4440 | 79250080 (9007, 9008) | Novel Protein sim. GBank gil 77319 dbj BAA08787 - (D50083) BUL1 [Saccharomyces cerevisiae] | UNCLASSIFIED | 1003, 1029 |
| 4441 | 25314591 (9347, 9348) | Novel Protein sim. GBank gil 77319 dbj BAA08787 - (D50083) BUL1 [Saccharomyces cerevisiae] | UNCLASSIFIED | 1009 |
| 4442 | 37030000 (3569, 3570) | Novel Protein sim. GBank gil 790910 L41861 - putative [Pseudomonas syringae] | UNCLASSIFIED | 1038 |

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| 4443 | 66177808 (4233, 4234) | Novel Protein sim. GBank gi 79557 pir S04678 - hypothetical protein 8 - Rhodopseudomonas blastic 2. (fragment) | | UNCLASSIFIED | 1022 |
| 4444 | 79618924 (10463, 10464) | Novel Protein sim. GBank gi 79973 pir S05542 - hypothetical protein, 54K - Enterococcus faecium | | UNCLASSIFIED | 1006 |
| 4445 | 16842116 (19533, 19534) | Novel Protein sim. GBank gi 807677 (M13101) - unknown protein [Rattus norvegicus] | | UNCLASSIFIED | 1008 |
| 4446 | 79253361 (22269, 22270) | Novel Protein sim. GBank gi 807677 (M13101) - unknown protein [Rattus norvegicus] | | UNCLASSIFIED | 1024 |
| 4447 | 78968384 (213, 214) | Novel Protein sim. GBank gi 81286 pir S22697 - extensin - Volvox carteri (fragment) | | UNCLASSIFIED | 1003 |
| 4448 | 28459036 (8915, 8916) | Novel Protein sim. GBank gi 81286 pir S22697 - extensin - Volvox carteri (fragment) | | UNCLASSIFIED | 1004, 1022, 1023, 1024, 1034 |
| 4449 | 78459239 (15465, 15466) | Novel Protein sim. GBank gi 81286 pir S22697 - extensin - Volvox carteri (fragment) | | UNCLASSIFIED | 1026 |
| 4450 | 79921163 (8027, 8028) | Novel Protein sim. GBank gi 825501 (L42348) - HO1 [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1008, 1023, 1039 |
| 4451 | 13502705 (1543, 1544) | Novel Protein sim. GBank gi 8333812 (U21643) - high-affinity glutamine permease [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1006 |
| 4452 | 81745594 (1969, 1970) | Novel Protein sim. GBank gi 840656 (L42524) - replication initiator and transcription repressor [Plasmid pSM500] | | UNCLASSIFIED | 1054 |
| 4453 | 80026632 (9491, 9492) | Novel Protein sim. GBank gi 845686 (M32103) - ORF-27 [Staphylococcus aureus] | | UNCLASSIFIED | 1006, 1026, 1027, 1029, 1053 |
| 4454 | 65876460 (1123, 1124) | Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6] | | UNCLASSIFIED | 1044 |
| 4455 | 79796417 (1189, 1190) | Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6] | | UNCLASSIFIED | 1004, 1006, 1008, 1017, 1023, 1024, 1034, 1039, 1044, 1054 |
| 4456 | 37420757 (2709, 2710) | Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6] | | UNCLASSIFIED | 1016 |

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| 4457 | 20021358 (4955, 4956) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1022 |
| 4458 | 28993067 (6277, 6278) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1017 |
| 4459 | 10144718 (7217, 7218) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1034 |
| 4460 | 78798207 (7601, 7602) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1026 |
| 4461 | 65890895 (7633, 7634) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1038 |
| 4462 | 79864042 (7631, 7832) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1017 |
| 4463 | 80085583 (11203, 11204) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1001 |
| 4464 | 55307020 (11849, 11850) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1019 |
| 4465 | 10119836 (11897, 11898) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1044 |
| 4466 | 32119969 (12717, 12718) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1044 |
| 4467 | 19521359 (13535, 13536) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1034 |
| 4468 | 80047867 (16109, 16110) | Novel Protein sim. G-Bank gi 854065 emb CAA58337 - (X83413) U88 [Human Herpesvirus 6] | | UNCLASSIFIED | 1023, 1024 |

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| 4469 | 78495393 (20715, 20716) | Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6] | | UNCLASSIFIED | 1038 |
| 4470 | 79586116 (21721, 21722) | Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6] | | UNCLASSIFIED | 1054 |
| 4471 | 65479236 (22503, 22504) | Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6] [Human herpesvirus 6] | | UNCLASSIFIED | 1054 |
| 4472 | 80257959 (22603, 22604) | Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6] | | UNCLASSIFIED | 1006 |
| 4473 | 81572628 (4435, 4436) | Novel Protein sim. GBank gi 85719 pir A40333 - collagen alpha 1(II) chain precursor - African clawed frog | | UNCLASSIFIED | 1001, 1003, 1008, 1016, 1023, 1024, 1029, 1044, 1054 |
| 4474 | 46872841 (5797, 5798) | Novel Protein sim. GBank gi 861277 (U28739) - C17G10.1 [Caenorhabditis elegans] | | UNCLASSIFIED | 1029 |
| 4475 | 80027777 (2523, 2524) | Novel Protein sim. GBank gi 87765 pir JU0033 - hypothetical L1 protein (third intron of gene TS) - human | | UNCLASSIFIED | 1004 |
| 4476 | 87452835 (5429, 5430) | Novel Protein sim. GBank gi 87765 pir JU0033 - hypothetical L1 protein (third intron of gene TS) - human | | UNCLASSIFIED | 1018 |
| 4477 | 78470339 (22567, 22568) | Novel Protein sim. GBank gi 882509 (U28377) - ORF >274 [Escherichia coli] | | UNCLASSIFIED | 1026 |
| 4478 | 80250942 (1139, 1140) | Novel Protein sim. GBank gi 882649 (U29579) - ORF >199 [Escherichia coli] | | UNCLASSIFIED | 1022, 1024 |
| 4479 | 79801250 (9887, 9888) | Novel Protein sim. GBank gi 886038 (U24689) - JadR1 [Streptomyces venezuelae] | | UNCLASSIFIED | 1017 |
| 4480 | 80481695 (18875, 18876) | Novel Protein sim. GBank gi 886319 (L39923) - ORF278; hypothetical 30.3 kd protein; similar to hypothetical protein 27.5 kd in SP00J-GDB Intergenic region of <i>B. subtilis</i> and to 27.5 kd protein in GIDB-UNC1 Intergenic region of <i>P.</i> <i>putida</i> ; putative [Mycobacterium leprae] | | UNCLASSIFIED | 1012 |

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| 4481 | 8373624 (16975, 16976) | Novel Protein sim. GBank gi 887833 (U28375) - ORF o439 [Escherichia coli] | | UNCLASSIFIED | 1003, 1026 |
| 4482 | 78834904 (6181, 6182) | Novel Protein sim. GBank gi 90157 pir A25345 - troponin T, cardiac muscle, major isoform - rabbit | | UNCLASSIFIED | 1019, 1021, 1029 |
| 4483 | 80402736 (13531, 13532) | Novel Protein sim. GBank gi 91210 pir B2424 - proline-rich protein MP3 - mouse (fragment) | | UNCLASSIFIED | 1022 |
| 4484 | 27977012 (22485, 22486) | Novel Protein sim. GBank gi 950682 (L38824) - putative [Plasmid R478] | | UNCLASSIFIED | 1010 |
| 4485 | 20466532 (10357, 10358) | Novel Protein sim. GBank gi 95489 pir C33830 - Alcaligenes eutrophus membrane protein czzC - cation efflux system | | UNCLASSIFIED | 1008, 1054 |
| 4486 | 85805102 (18595, 18596) | Novel Protein sim. GBank gi 95690 pir S14411 - carbon starvation protein - Escherichia coli | | UNCLASSIFIED | 1017 |
| 4487 | 18589572 (11211, 11212) | Novel Protein sim. GBank gi 96522 pir A36129 - trigger factor - Escherichia coli | | UNCLASSIFIED | 1006 |
| 4488 | 11090399 (2769, 2770) | Novel Protein sim. GBank gi 973332 (U30873) - OrfC [Bacillus subtilis] | | UNCLASSIFIED | |
| 4489 | 65680528 (17141, 17142) | Novel Protein sim. GBank gi 97476 pir S19740 - hypothetical protein B - Rhodobacter capsulatus | | UNCLASSIFIED | 1010 |
| 4490 | 20438222 (5273, 5274) | Novel Protein sim. GBank gi 97480 pir S19739 - integral membrane protein - Rhodobacter capsulatus | | UNCLASSIFIED | 1010 |
| 4491 | 78399485 (10821, 10822) | Novel Protein sim. GBank gi 984814 (U27196) - zinc finger protein [Gallus gallus] | | UNCLASSIFIED | 1038 |
| 4492 | 20285233 (11621, 11622) | Novel Protein sim. GBank gi 98773 pir S22630 - 19K antigen - Mycobacterium intracellulare | | UNCLASSIFIED | 1034 |
| 4493 | 80245788 (9659, 9660) | Novel Protein sim. GBank gi 98810 pir S21833 - hypothetical protein - Mycobacterium tuberculosis | | UNCLASSIFIED | 1004, 1006, 1022, 1024, 1044, 1050 |
| 4494 | 79833913 (2961, 2962) | Novel Protein sim. GBank gi 995573 (U03772) - putative transposase [Acinetobacter sp. ADP1] | | UNCLASSIFIED | 1008 |
| 4495 | 11269481 (9641, 9642) | Novel Protein sim. GBank gi 985714 emb [CA A62663] - (X91258) L3177 [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1010 |
| 4496 | 9846880 (5, 6) | | | UNCLASSIFIED | 1008 |

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| 4497 | 65493874 (13, 14) | | UNCLASSIFIED | 1023 |
| 4498 | 29249693 (19, 20) | | UNCLASSIFIED | 1026 |
| 4499 | 35066762 (27, 28) | | UNCLASSIFIED | 1054 |
| 4500 | 20287804 (31, 32) | | UNCLASSIFIED | 1034 |
| 4501 | 86689310 (39, 40) | | UNCLASSIFIED | 1001, 1025 |
| 4502 | 78491874 (47, 48) | | UNCLASSIFIED | 1054 |
| 4503 | 25264471 (53, 54) | | UNCLASSIFIED | 1039 |
| 4504 | 79796056 (61, 62) | | UNCLASSIFIED | 1044 |
| 4505 | 79634543 (79, 80) | | UNCLASSIFIED | 1025 |
| 4506 | 20617182 (85, 86) | | UNCLASSIFIED | 1004 |
| 4507 | 79183388 (87, 88) | | UNCLASSIFIED | 1031 |
| 4508 | 70437139 (91, 92) | | UNCLASSIFIED | 1041 |
| 4509 | 38905642 (93, 94) | | UNCLASSIFIED | 1026 |
| 4510 | 80481704 (95, 96) | | UNCLASSIFIED | 1012 |
| 4511 | 94323105 (101, 102) | | UNCLASSIFIED | 1054 |
| 4512 | 94137362 (103, 104) | | UNCLASSIFIED | 1013, 1042, 1044 |
| 4513 | 17884908 (109, 110) | | UNCLASSIFIED | 1024 |
| 4514 | 38069116 (111, 112) | | UNCLASSIFIED | 1054 |

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| 4515 | 65689631 (113, 114), | | | UNCLASSIFIED | 1053 |
| 4516 | 79600369 (115, 116), | | | UNCLASSIFIED | 1006 |
| 4517 | 78380394 (121, 122), | | | UNCLASSIFIED | 1008, 1026, 1029 |
| 4518 | 29881396 (129, 130) | | | UNCLASSIFIED | 1038 |
| 4519 | 27975422 (145, 146) | | | UNCLASSIFIED | 1053 |
| 4520 | 20417383 (149, 150), | | | UNCLASSIFIED | 1004 |
| 4521 | 49609065 (155, 156), | | | UNCLASSIFIED | 1040 |
| 4522 | 30797666 (157, 158), | | | UNCLASSIFIED | 1026 |
| 4523 | 39527189 (161, 162), | | | UNCLASSIFIED | 1006 |
| 4524 | 11685039 (163, 164), | | | UNCLASSIFIED | 1016 |
| 4525 | 79638103 (169, 170), | | | UNCLASSIFIED | 1025, 1038 |
| 4526 | 85818238 (171, 172), | | | UNCLASSIFIED | 1019 |
| 4527 | 65464571 (173, 174), | | | UNCLASSIFIED | 1049 |
| 4528 | 25259756 (177, 178), | | | UNCLASSIFIED | 1008 |
| 4529 | 36897891 (203, 204), | | | UNCLASSIFIED | 1030 |
| 4530 | 66435382 (207, 208), | | | UNCLASSIFIED | 1024 |
| 4531 | 35902288 (221, 222), | | | UNCLASSIFIED | 1029 |
| 4532 | 79585126 (225, 226), | | | UNCLASSIFIED | 1022 |

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| 4533 | 11104197 (241, 242) | | | UNCLASSIFIED | 1053 |
| 4534 | 17899010 (247, 248) | | | UNCLASSIFIED | 1023 |
| 4535 | 27348004 (249, 250) | | | UNCLASSIFIED | 1009 |
| 4536 | 79777084 (251, 252) | | | UNCLASSIFIED | 1006, 1008 |
| 4537 | 30784847 (261, 262) | | | UNCLASSIFIED | 1003 |
| 4538 | 94853854 (285, 286) | | | UNCLASSIFIED | 1010, 1054 |
| 4539 | 10866996 (299, 300) | | | UNCLASSIFIED | 1034 |
| 4540 | 27965979 (305, 306) | | | UNCLASSIFIED | 1006 |
| 4541 | 17089664 (315, 316) | | | UNCLASSIFIED | 1038 |
| 4542 | 70445891 (347, 348) | | | UNCLASSIFIED | 1021, 1041 |
| 4543 | 66489680 (359, 360) | | | UNCLASSIFIED | 1029 |
| 4544 | 79625154 (361, 362) | | | UNCLASSIFIED | 1009, 1039 |
| 4545 | 87466598 (367, 368) | | | UNCLASSIFIED | 1015 |
| 4546 | 20730941 (389, 390) | | | UNCLASSIFIED | 1006 |
| 4547 | 78245845 (391, 392) | | | UNCLASSIFIED | 1050 |
| 4548 | 43155273 (399, 400) | | | UNCLASSIFIED | 1037 |
| 4549 | 77879730 (401, 402) | | | UNCLASSIFIED | 1018 |
| 4550 | 65892848 (403, 404) | | | UNCLASSIFIED | 1054 |

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| 4551 | 16335049 (423, 424) | | | UNCLASSIFIED | 1006 |
| 4552 | 77876576 (429, 430) | | | UNCLASSIFIED | 1019 |
| 4553 | 55402072 (453, 454) | | | UNCLASSIFIED | 1019 |
| 4554 | 78675447 (459, 460) | | | UNCLASSIFIED | 1008 |
| 4555 | 57302106 (483, 484) | | | UNCLASSIFIED | 1006, 1024 |
| 4556 | 20723641 (485, 486) | | | UNCLASSIFIED | 1006 |
| 4557 | 78793908 (487, 488) | | | UNCLASSIFIED | 1009 |
| 4558 | 65448002 (493, 494) | | | UNCLASSIFIED | 1009 |
| 4559 | 78193745 (495, 496) | | | UNCLASSIFIED | 1029 |
| 4560 | 79975683 (505, 506) | | | UNCLASSIFIED | 1025 |
| 4561 | 11090550 (511, 512) | | | UNCLASSIFIED | 1006 |
| 4562 | 32094039 (513, 514) | | | UNCLASSIFIED | 1044 |
| 4563 | 79853796 (527, 528) | | | UNCLASSIFIED | 1023 |
| 4564 | 78922935 (529, 530) | | | UNCLASSIFIED | 1039 |
| 4565 | 32444528 (531, 532) | | | UNCLASSIFIED | 1029 |
| 4566 | 27977688 (539, 540) | | | UNCLASSIFIED | 1006 |
| 4567 | 80062542 (543, 544) | | | UNCLASSIFIED | 1010 |
| 4568 | 66936028 (545, 546) | | | UNCLASSIFIED | 1019, 1049 |

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| 4569 | 8474093 (553, 554) | | UNCLASSIFIED | 1034 |
| 4570 | 29357849 (569, 570) | | UNCLASSIFIED | 1023 |
| 4571 | 20635625 (573, 574) | | UNCLASSIFIED | 1022 |
| 4572 | 11090554 (601, 602) | | UNCLASSIFIED | 1006 |
| 4573 | 38191553 (605, 606) | | UNCLASSIFIED | 1008 |
| 4574 | 13085136 (607, 608) | | UNCLASSIFIED | 1024 |
| 4575 | 79549190 (611, 612) | | UNCLASSIFIED | 1038 |
| 4576 | 20433843 (641, 642) | | UNCLASSIFIED | 1024 |
| 4577 | 19431094 (649, 650) | | UNCLASSIFIED | 1003 |
| 4578 | 32601107 (651, 652) | | UNCLASSIFIED | 1034 |
| 4579 | 79561278 (693, 694) | | UNCLASSIFIED | 1038 |
| 4580 | 20462931 (713, 714) | | UNCLASSIFIED | 1001, 1034 |
| 4581 | 80093083 (715, 716) | | UNCLASSIFIED | 1054 |
| 4582 | 80034797 (723, 724) | | UNCLASSIFIED | 1053 |
| 4583 | 55308623 (729, 730) | | UNCLASSIFIED | 1012, 1042 |
| 4584 | 71088722 (731, 732) | | UNCLASSIFIED | 1053 |
| 4585 | 35101923 (745, 746) | | UNCLASSIFIED | 1024 |
| 4586 | 10252060 (759, 760) | | UNCLASSIFIED | 1038 |

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| 4587 | 8517446 (765, 766) | | | UNCLASSIFIED | 1022 |
| 4588 | 94315340 (767, 768) | | | UNCLASSIFIED | 1003 |
| 4589 | 79592603 (769, 770) | | | UNCLASSIFIED | 1010 |
| 4590 | 78299571 (775, 776) | | | UNCLASSIFIED | 1026 |
| 4591 | 19887951 (787, 788) | | | UNCLASSIFIED | 1001 |
| 4592 | 79954360 (793, 794) | | | UNCLASSIFIED | 1025 |
| 4593 | 17302392 (795, 796) | | | UNCLASSIFIED | 1008 |
| 4594 | 77654893 (805, 806) | | | UNCLASSIFIED | 1024 |
| 4595 | 79624224 (813, 814) | | | UNCLASSIFIED | 1023 |
| 4596 | 46806799 (817, 818) | | | UNCLASSIFIED | 1041 |
| 4597 | 80066630 (829, 830) | | | UNCLASSIFIED | 1024, 1054 |
| 4598 | 57666192 (831, 832) | | | UNCLASSIFIED | 1051 |
| 4599 | 65896665 (835, 836) | | | UNCLASSIFIED | 1054 |
| 4600 | 29213531 (849, 850) | | | UNCLASSIFIED | 1044 |
| 4601 | 84877446 (877, 878) | | | UNCLASSIFIED | 1022 |
| 4602 | 17690652 (879, 880) | | | UNCLASSIFIED | 1039 |
| 4603 | 16841330 (885, 886) | | | UNCLASSIFIED | 1044 |
| 4604 | 30258305 (911, 912) | | | UNCLASSIFIED | 1008 |

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| 4605 | 30243801 (927, 928) | | | UNCLASSIFIED | 1026 |
| 4606 | 80188879 (937, 938) | | | UNCLASSIFIED | 1022, 1058 |
| 4607 | 81777196 (961, 962) | | | UNCLASSIFIED | 1003, 1010, 1024 |
| 4608 | 20610456 (981, 982) | | | UNCLASSIFIED | 1004 |
| 4609 | 79578027 (985, 986) | | | UNCLASSIFIED | 1006 |
| 4610 | 35606134 (997, 998) | | | UNCLASSIFIED | 1053 |
| 4611 | 33711024 (1001, 1002) | | | UNCLASSIFIED | 1034 |
| 4612 | 90937181 (1009, 1010) | | | UNCLASSIFIED | 1008, 1017, 1020, 1054 |
| 4613 | 29444464 (1013, 1014) | | | UNCLASSIFIED | 1026 |
| 4614 | 8026194 (1029, 1030) | | | UNCLASSIFIED | 1010, 1017, 1023, 1034, 1039 |
| 4615 | 21417118 (1037, 1038) | | | UNCLASSIFIED | 1034 |
| 4616 | 20293187 (1041, 1042) | | | UNCLASSIFIED | 1034 |
| 4617 | 11689569 (1067, 1068) | | | UNCLASSIFIED | 1034 |
| 4618 | 11594236 (1077, 1078) | | | UNCLASSIFIED | 1034 |
| 4619 | 66596127 (1087, 1088) | | | UNCLASSIFIED | 1008, 1050 |
| 4620 | 20294715 (1091, 1092) | | | UNCLASSIFIED | 1034 |
| 4621 | 27826749 (1097, 1098) | | | UNCLASSIFIED | 1004 |
| 4622 | 11311200 (1101, 1102) | | | UNCLASSIFIED | 1004 |

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| 4623 | 66432596 (1129, 1130) | | UNCLASSIFIED | 1003, 1024 |
| 4624 | 33188191 (1131, 1132) | | UNCLASSIFIED | 1026 |
| 4625 | 19515516 (1147, 1148) | | UNCLASSIFIED | 1010 |
| 4626 | 95287728 (1153, 1154) | | UNCLASSIFIED | 1012 |
| 4627 | 65687079 (1155, 1156) | | UNCLASSIFIED | 1049 |
| 4628 | 10318131 (1159, 1160) | | UNCLASSIFIED | 1025 |
| 4629 | 65507263 (1163, 1164) | | UNCLASSIFIED | 1016 |
| 4630 | 11090012 (1169, 1170) | | UNCLASSIFIED | 1004 |
| 4631 | 79207956 (1187, 1188) | | UNCLASSIFIED | 1054 |
| 4632 | 10167111 (1203, 1204) | | UNCLASSIFIED | 1001 |
| 4633 | 79111413 (1227, 1228) | | UNCLASSIFIED | 1008, 1023, 1039 |
| 4634 | 30802163 (1235, 1236) | | UNCLASSIFIED | 1029 |
| 4635 | 10184774 (1251, 1252) | | UNCLASSIFIED | 1003 |
| 4636 | 78368100 (1261, 1262) | | UNCLASSIFIED | 1008 |
| 4637 | 57108817 (1285, 1286) | | UNCLASSIFIED | 1001 |
| 4638 | 11171532 (1287, 1288) | | UNCLASSIFIED | 1022 |
| 4639 | 20617923 (1307, 1308) | | UNCLASSIFIED | 1022 |
| 4640 | 42942388 (1315, 1316) | | UNCLASSIFIED | 1000 |

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| | | | UNCLASSIFIED | 1009 |
| 4641 | 24135956 (1327, 1328) | | UNCLASSIFIED | 1003 |
| 4642 | 25133369 (1329, 1330) | | UNCLASSIFIED | 1029 |
| 4643 | 37013769 (1331, 1332) | | UNCLASSIFIED | 1003 |
| 4644 | 25266291 (1337, 1338) | | UNCLASSIFIED | 1004 |
| 4645 | 20632797 (1339, 1340) | | UNCLASSIFIED | 1054 |
| 4646 | 65897765 (1345, 1346) | | UNCLASSIFIED | 1044 |
| 4647 | 78902794 (1351, 1352) | | UNCLASSIFIED | 1037 |
| 4648 | 42392967 (1353, 1354) | | UNCLASSIFIED | 1053 |
| 4649 | 8720829 (1357, 1358) | | UNCLASSIFIED | 1038 |
| 4650 | 37030710 (1371, 1372) | | UNCLASSIFIED | 1004 |
| 4651 | 20619152 (1385, 1386) | | UNCLASSIFIED | 1024 |
| 4652 | 28916453 (1389, 1390) | | UNCLASSIFIED | 1009 |
| 4653 | 28498389 (1393, 1394) | | UNCLASSIFIED | 1026 |
| 4654 | 78252926 (1397, 1398) | | UNCLASSIFIED | 1023 |
| 4655 | 77593493 (1405, 1406) | | UNCLASSIFIED | 1034 |
| 4656 | 80207649 (1407, 1408) | | UNCLASSIFIED | 1038, 1039 |
| 4657 | 80428752 (1409, 1410) | | UNCLASSIFIED | 1023 |
| 4658 | 25167576 (1447, 1448) | | UNCLASSIFIED | |

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| 4659 | 27972165 (1451, 1452) | | UNCLASSIFIED | 1006 |
| 4660 | 56303804 (1473, 1474) | | UNCLASSIFIED | 1016 |
| 4661 | 78254851 (1475, 1476) | | UNCLASSIFIED | 1026 |
| 4662 | 77706453 (1481, 1482) | | UNCLASSIFIED | 1044 |
| 4663 | 15031765 (1483, 1484) | | UNCLASSIFIED | 1054 |
| 4664 | 11359941 (1501, 1502) | | UNCLASSIFIED | 1006 |
| 4665 | 79866321 (1503, 1504) | | UNCLASSIFIED | 1038 |
| 4666 | 39564900 (1519, 1520) | | UNCLASSIFIED | 1022, 1024 |
| 4667 | 18234054 (1541, 1542) | | UNCLASSIFIED | 1024 |
| 4668 | 51620195 (1545, 1546) | | UNCLASSIFIED | 1040 |
| 4669 | 28799635 (1547, 1548) | | UNCLASSIFIED | 1022 |
| 4670 | 80236214 (1549, 1550) | | UNCLASSIFIED | 1006 |
| 4671 | 78908513 (1553, 1554) | | UNCLASSIFIED | 1003, 1039 |
| 4672 | 17890206 (1557, 1558) | | UNCLASSIFIED | 1025 |
| 4673 | 47656276 (1565, 1566) | | UNCLASSIFIED | 1029 |
| 4674 | 33204747 (1573, 1574) | | UNCLASSIFIED | 1026 |
| 4675 | 78467565 (1575, 1576) | | UNCLASSIFIED | 1008 |
| 4676 | 79584957 (1577, 1578) | | UNCLASSIFIED | 1054 |

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| 4677 | 29946342 (1587, 1588) | | UNCLASSIFIED | 1038 |
| 4678 | 37015719 (1601, 1602) | | UNCLASSIFIED | 1029 |
| 4679 | 85544086 (1613, 1614) | | UNCLASSIFIED | 1016, 1034, 1038, |
| 4680 | 55404303 (1615, 1616) | | UNCLASSIFIED | 1041 |
| 4681 | 55658487 (1617, 1618) | | UNCLASSIFIED | 1021 |
| 4682 | 46873136 (1627, 1628) | | UNCLASSIFIED | 1042 |
| 4683 | 65880999 (1629, 1630) | | UNCLASSIFIED | 1050 |
| 4684 | 17682849 (1635, 1636) | | UNCLASSIFIED | 1039 |
| 4685 | 36824627 (1659, 1660) | | UNCLASSIFIED | 1054 |
| 4686 | 17702485 (1669, 1670) | | UNCLASSIFIED | 1003 |
| 4687 | 78733265 (1673, 1674) | | UNCLASSIFIED | 1026, 1050 |
| 4688 | 66155223 (1677, 1678) | | UNCLASSIFIED | 1003 |
| 4689 | 16345558 (1685, 1686) | | UNCLASSIFIED | 1022 |
| 4690 | 79232662 (1687, 1688) | | UNCLASSIFIED | 1003, 1023 |
| 4691 | 80380078 (1691, 1692) | | UNCLASSIFIED | 1001, 1017, 1024, 1029 |
| 4692 | 3253701 (1709, 1710) | | UNCLASSIFIED | 1034 |
| 4693 | 54700090 (1715, 1716) | | UNCLASSIFIED | 1019 |
| 4694 | 10067522 (1727, 1728) | | UNCLASSIFIED | 1012 |

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| 4695 | 79640542 (1731, 1732) | | | UNCLASSIFIED | 1025 |
| 4696 | 35062253 (1733, 1734) | | | UNCLASSIFIED | 1024 |
| 4697 | 13519751 (1743, 1744) | | | UNCLASSIFIED | 1024 |
| 4698 | 80236216 (1745, 1746) | | | UNCLASSIFIED | 1006, 1017 |
| 4699 | 94328999 (1759, 1760) | | | UNCLASSIFIED | 1010 |
| 4700 | 78928034 (1767, 1768) | | | UNCLASSIFIED | 1008, 1050 |
| 4701 | 85519710 (1773, 1774) | | | UNCLASSIFIED | 1003, 1023, 1049, 1058 |
| 4702 | 78360920 (1785, 1786) | | | UNCLASSIFIED | 1008, 1026 |
| 4703 | 78823898 (1789, 1790) | | | UNCLASSIFIED | 1016, 1054 |
| 4704 | 54537001 (1797, 1798) | | | UNCLASSIFIED | 1041 |
| 4705 | 94239569 (1799, 1800) | | | UNCLASSIFIED | 1039 |
| 4706 | 35106845 (1809, 1810) | | | UNCLASSIFIED | 1026 |
| 4707 | 20451074 (1817, 1818) | | | UNCLASSIFIED | 1024 |
| 4708 | 36827848 (1819, 1820) | | | UNCLASSIFIED | 1054 |
| 4709 | 79642387 (1827, 1828) | | | UNCLASSIFIED | 1022, 1038 |
| 4710 | 19456885 (1833, 1834) | | | UNCLASSIFIED | 1038 |
| 4711 | 10365133 (1843, 1844) | | | UNCLASSIFIED | 1001 |
| 4712 | 70760933 (1847, 1848) | | | UNCLASSIFIED | 1034 |

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| 4713 | 80025927 (1856, 1856) | | UNCLASSIFIED | 1004, 1006, 1024, |
| 4714 | 79115173 (1871, 1872) | | UNCLASSIFIED | 1003 |
| 4715 | 36921063 (1875, 1876) | | UNCLASSIFIED | 1026 |
| 4716 | 23291629 (1887, 1888) | | UNCLASSIFIED | 1003 |
| 4717 | 38879543 (1899, 1900) | | UNCLASSIFIED | 1019 |
| 4718 | 65890856 (1903, 1904) | | UNCLASSIFIED | 1038 |
| 4719 | 35062838 (1909, 1910) | | UNCLASSIFIED | 1024 |
| 4720 | 38909591 (1937, 1938) | | UNCLASSIFIED | 1024 |
| 4721 | 65488001 (1943, 1944) | | UNCLASSIFIED | 1023 |
| 4722 | 29207312 (1947, 1948) | | UNCLASSIFIED | 1030 |
| 4723 | 80407444 (1965, 1966) | | UNCLASSIFIED | 1003, 1008, 1023, 1026, 1029, 1044, 1053 |
| 4724 | 21662567 (1999, 2000) | | UNCLASSIFIED | 1024, 1038, 1054 |
| 4725 | 29228558 (2021, 2022) | | UNCLASSIFIED | 1030 |
| 4726 | 79959396 (2023, 2024) | | UNCLASSIFIED | 1016 |
| 4727 | 79201769 (2029, 2030) | | UNCLASSIFIED | 1001, 1025, 1044, 1054 |
| 4728 | 20417013 (2057, 2058) | | UNCLASSIFIED | 1004 |
| 4729 | 20752080 (2067, 2068) | | UNCLASSIFIED | 1022 |
| 4730 | 79480166 (2069, 2070) | | UNCLASSIFIED | 1025 |

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| 4731 | 20750859 (2071, 2072) | | | |
| 4732 | 16841981 (2083, 2084) | | UNCLASSIFIED | 1039 |
| 4733 | 78375158 (2085, 2086) | | UNCLASSIFIED | 1003 |
| 4734 | 80076596 (2095, 2096) | | UNCLASSIFIED | 1022 |
| 4735 | 80025928 (2099, 2100) | | UNCLASSIFIED | 1006, 1010, 1034 |
| 4736 | 29017297 (2103, 2104) | | UNCLASSIFIED | 1044 |
| 4737 | 30800379 (2109, 2110) | | UNCLASSIFIED | 1006 |
| 4738 | 78890648 (2123, 2124) | | UNCLASSIFIED | 1044 |
| 4739 | 78460233 (2125, 2126) | | UNCLASSIFIED | 1026 |
| 4740 | 66148000 (2151, 2152) | | UNCLASSIFIED | 1038 |
| 4741 | 91230908 (2159, 2160) | | UNCLASSIFIED | 1003 |
| 4742 | 46850003 (2161, 2162) | | UNCLASSIFIED | 1029 |
| 4743 | 71466607 (2167, 2168) | | UNCLASSIFIED | 1026 |
| 4744 | 16423261 (2177, 2178) | | UNCLASSIFIED | 1016 |
| 4745 | 39565694 (2181, 2182) | | UNCLASSIFIED | 1010 |
| 4746 | 10872205 (2189, 2190) | | UNCLASSIFIED | 1004 |
| 4747 | 79201928 (2199, 2200) | | UNCLASSIFIED | 1024 |
| 4748 | 78399033 (2201, 2202) | | UNCLASSIFIED | 1038 |

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| 4749 | 36921068 (2205, 2206) | | UNCLASSIFIED | 1028 |
| 4750 | 78677359 (2215, 2216) | | UNCLASSIFIED | 1026 |
| 4751 | 71761302 (2221, 2222) | | UNCLASSIFIED | 1026 |
| 4752 | 17277231 (2223, 2224) | | UNCLASSIFIED | 1008 |
| 4753 | 78167568 (2225, 2226) | | UNCLASSIFIED | 1000 |
| 4754 | 78191615 (2227, 2228) | | UNCLASSIFIED | 1024 |
| 4755 | 20437153 (2231, 2232) | | UNCLASSIFIED | 1010 |
| 4756 | 17668990 (2241, 2242) | | UNCLASSIFIED | 1008 |
| 4757 | 29916352 (2251, 2252) | | UNCLASSIFIED | 1030 |
| 4758 | 78068607 (2261, 2262) | | UNCLASSIFIED | 1001 |
| 4759 | 29457545 (2271, 2272) | | UNCLASSIFIED | 1022 |
| 4760 | 54697548 (2273, 2274) | | UNCLASSIFIED | 1022 |
| 4761 | 34669099 (2279, 2280) | | UNCLASSIFIED | 1024 |
| 4762 | 25256289 (2283, 2284) | | UNCLASSIFIED | 1008 |
| 4763 | 79629028 (2291, 2292) | | UNCLASSIFIED | 1039 |
| 4764 | 41083545 (2295, 2296) | | UNCLASSIFIED | 1037 |
| 4765 | 19512872 (2297, 2298) | | UNCLASSIFIED | 1010 |
| 4766 | 94680343 (2307, 2308) | | UNCLASSIFIED | 1009, 1024, 1031 |

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| | | | UNCLASSIFIED | 1024 |
| 4767 | 8485740 (2309, 2310), | | UNCLASSIFIED | 1036 |
| 4768 | 77891859 (2313, 2314) | | UNCLASSIFIED | 1036 |
| 4769 | 65846664 (2315, 2316) | | UNCLASSIFIED | 1038 |
| 4770 | 65881051 (2331, 2332) | | UNCLASSIFIED | 1044 |
| 4771 | 11695127 (2339, 2340) | | UNCLASSIFIED | 1006 |
| 4772 | 86695575 (2349, 2350) | | UNCLASSIFIED | 1022, 1034, 1038 |
| 4773 | 91213648 (2367, 2368) | | UNCLASSIFIED | 1024 |
| 4774 | 80243819 (2385, 2386) | | UNCLASSIFIED | 1022, 1044 |
| 4775 | 27844078 (2387, 2388) | | UNCLASSIFIED | 1024, 1034 |
| 4776 | 20296623 (2391, 2392) | | UNCLASSIFIED | 1034 |
| 4777 | 79245600 (2409, 2410) | | UNCLASSIFIED | 1024, 1039 |
| 4778 | 78914507 (2411, 2412) | | UNCLASSIFIED | 1039 |
| 4779 | 12999306 (2415, 2416) | | UNCLASSIFIED | 1024 |
| 4780 | 38348356 (2425, 2426) | | UNCLASSIFIED | 1008 |
| 4781 | 11670394 (2431, 2432) | | UNCLASSIFIED | 1016, 1022 |
| 4782 | 80063162 (2449, 2450) | | UNCLASSIFIED | 1010, 1022, 1024, 1026, 1038 |
| 4783 | 79258057 (2477, 2478) | | UNCLASSIFIED | 1003 |
| 4784 | 11092879 (2479, 2480) | | UNCLASSIFIED | 1022 |

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| 4785 | 11776390 (2483, 2484) | | UNCLASSIFIED | 1006 |
| 4786 | 65882019 (2491, 2492) | | UNCLASSIFIED | 1054 |
| 4787 | 51782563 (2499, 2500) | | UNCLASSIFIED | 1038, 1042 |
| 4788 | 78473417 (2515, 2516) | | UNCLASSIFIED | 1026 |
| 4789 | 87898974 (2537, 2538) | | UNCLASSIFIED | 1015, 1022, 1025 |
| 4790 | 9398491 (2539, 2540) | | UNCLASSIFIED | 1017 |
| 4791 | 28382878 (2541, 2542) | | UNCLASSIFIED | 1017 |
| 4792 | 20284772 (2545, 2546) | | UNCLASSIFIED | 1022 |
| 4793 | 11290122 (2557, 2558) | | UNCLASSIFIED | 1034 |
| 4794 | 25310199 (2567, 2568) | | UNCLASSIFIED | 1003 |
| 4795 | 86667225 (2571, 2572) | | UNCLASSIFIED | 1029 |
| 4796 | 20285338 (2579, 2580) | | UNCLASSIFIED | 1022 |
| 4797 | 79830272 (2581, 2582) | | UNCLASSIFIED | 1039 |
| 4798 | 11122661 (2587, 2588) | | UNCLASSIFIED | 1053 |
| 4799 | 78918477 (2597, 2598) | | UNCLASSIFIED | 1039 |
| 4800 | 20287821 (2599, 2600) | | UNCLASSIFIED | 1034 |
| 4801 | 23294346 (2601, 2602) | | UNCLASSIFIED | 1044 |
| 4802 | 95010589 (2605, 2606) | | UNCLASSIFIED | 1024, 1034, 1039 |

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| 4803 | 65859051 (2607, 2608) | | UNCLASSIFIED | 1038 |
| 4804 | 34755701 (2609, 2610) | | UNCLASSIFIED | 1030 |
| 4805 | 42563732 (2611, 2612) | | UNCLASSIFIED | 1000, 1034 |
| 4806 | 65891738 (2613, 2614) | | UNCLASSIFIED | 1054 |
| 4807 | 11707335 (2619, 2620) | | UNCLASSIFIED | 1038 |
| 4808 | 86723375 (2625, 2626) | | UNCLASSIFIED | 1001, 1018 |
| 4809 | 47657344 (2641, 2642) | | UNCLASSIFIED | 1029 |
| 4810 | 87125822 (2659, 2660) | | UNCLASSIFIED | 1048 |
| 4811 | 21669817 (2661, 2662) | | UNCLASSIFIED | 1024 |
| 4812 | 30370208 (2673, 2674) | | UNCLASSIFIED | 1054 |
| 4813 | 1292917 (2689, 2690) | | UNCLASSIFIED | 1024 |
| 4814 | 78464624 (2715, 2716) | | UNCLASSIFIED | 1039 |
| 4815 | 78674394 (2739, 2740) | | UNCLASSIFIED | 1009 |
| 4816 | 79855987 (2741, 2742) | | UNCLASSIFIED | 1017, 1044 |
| 4817 | 65683598 (2743, 2744) | | UNCLASSIFIED | 1046 |
| 4818 | 79910981 (2745, 2746) | | UNCLASSIFIED | 1001, 1010, 1038 |
| 4819 | 65888420 (2747, 2748) | | UNCLASSIFIED | 1054 |
| 4820 | 65893010 (2765, 2766) | | UNCLASSIFIED | 1054 |

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| 4821 | 78793103 (2805, 2806) | | UNCLASSIFIED | 1044 |
| 4822 | 79480342 (2807, 2808) | | UNCLASSIFIED | 1022 |
| 4823 | 86380873 (2813, 2814) | | UNCLASSIFIED | 1053 |
| 4824 | 87890180 (2815, 2816) | | UNCLASSIFIED | 1015 |
| 4825 | 29361964 (2823, 2824) | | UNCLASSIFIED | 1023 |
| 4826 | 79625167 (2847, 2848) | | UNCLASSIFIED | 1023 |
| 4827 | 80200419 (2861, 2862) | | UNCLASSIFIED | 1034 |
| 4828 | 51728608 (2873, 2874) | | UNCLASSIFIED | 1040 |
| 4829 | 65655505 (2889, 2890) | | UNCLASSIFIED | 1054 |
| 4830 | 10015425 (2909, 2910) | | UNCLASSIFIED | 1023 |
| 4831 | 24115387 (2911, 2912) | | UNCLASSIFIED | 1044 |
| 4832 | 11816407 (2915, 2916) | | UNCLASSIFIED | 1004 |
| 4833 | 78962233 (2919, 2920) | | UNCLASSIFIED | 1038 |
| 4834 | 80020135 (2921, 2922) | | UNCLASSIFIED | 1053 |
| 4835 | 37443826 (2927, 2928) | | UNCLASSIFIED | 1034 |
| 4836 | 30378685 (2943, 2944) | | UNCLASSIFIED | 1050 |
| 4837 | 30394718 (2945, 2946) | | UNCLASSIFIED | 1038 |
| 4838 | 27967298 (2951, 2952) | | UNCLASSIFIED | 1006 |

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| 4839 | 79450986 (2955, 2956) | | UNCLASSIFIED | 1016 |
| 4840 | 79626143 (2969, 2970) | | UNCLASSIFIED | 1025, 1054 |
| 4841 | 66258467 (2991, 2992) | | UNCLASSIFIED | 1010 |
| 4842 | 65503433 (2995, 2996) | | UNCLASSIFIED | 1049 |
| 4843 | 98863838 (3009, 3010) | | UNCLASSIFIED | 1008 |
| 4844 | 65981228 (3025, 3026) | | UNCLASSIFIED | 1024 |
| 4845 | 8501919 (3075, 3076) | | UNCLASSIFIED | 1022 |
| 4846 | 78918087 (3091, 3092) | | UNCLASSIFIED | 1008, 1034 |
| 4847 | 91236209 (3095, 3096) | | UNCLASSIFIED | 1045 |
| 4848 | 27351119 (3113, 3114) | | UNCLASSIFIED | 1009 |
| 4849 | 13042410 (3125, 3126) | | UNCLASSIFIED | 1004 |
| 4850 | 80499456 (3133, 3134) | | UNCLASSIFIED | 1012 |
| 4851 | 78366834 (3137, 3138) | | UNCLASSIFIED | 1003 |
| 4852 | 79806217 (3141, 3142) | | UNCLASSIFIED | 1022, 1034 |
| 4853 | 80503986 (3143, 3144) | | UNCLASSIFIED | 1006, 1012 |
| 4854 | 9850539 (3171, 3172) | | UNCLASSIFIED | 1039 |
| 4855 | 10858672 (3193, 3194) | | UNCLASSIFIED | 1031 |
| 4856 | 79620177 (3197, 3198) | | UNCLASSIFIED | 1025 |

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| 4857 | 27980198 (3231, 3232) | | UNCLASSIFIED | 1006 |
| 4858 | 65888269 (3237, 3238) | | UNCLASSIFIED | 1054 |
| 4859 | 94667164 (3261, 3262) | | UNCLASSIFIED | 1044 |
| 4860 | 65503812 (3265, 3266) | | UNCLASSIFIED | 1016 |
| 4861 | 78377906 (3267, 3268) | | UNCLASSIFIED | 1039 |
| 4862 | 28398655 (3279, 3280) | | UNCLASSIFIED | 1030, 1054 |
| 4863 | 94329389 (3287, 3288) | | UNCLASSIFIED | 1010 |
| 4864 | 85532538 (3289, 3290) | | UNCLASSIFIED | 1038 |
| 4865 | 10200245 (3299, 3300) | | UNCLASSIFIED | 1006 |
| 4866 | 13521875 (3301, 3302) | | UNCLASSIFIED | 1034 |
| 4867 | 29333200 (3309, 3310) | | UNCLASSIFIED | 1009 |
| 4868 | 33184749 (3311, 3312) | | UNCLASSIFIED | 1026 |
| 4869 | 21660695 (3321, 3322) | | UNCLASSIFIED | 1017, 1024 |
| 4870 | 79484179 (3327, 3328) | | UNCLASSIFIED | 1031 |
| 4871 | 80027391 (3337, 3338) | | UNCLASSIFIED | 1003, 1006, 1032 |
| 4872 | 11072274 (3353, 3354) | | UNCLASSIFIED | 1034 |
| 4873 | 36884820 (3363, 3364) | | UNCLASSIFIED | 1054 |
| 4874 | 95004965 (3365, 3366) | | UNCLASSIFIED | 1006, 1017, 1034 |

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| 4875 | 78376978 (3381, 3382) | | | UNCLASSIFIED | 1008 |
| 4876 | 11102092 (3383, 3384) | | | UNCLASSIFIED | 1053 |
| 4877 | 20596518 (3407, 3408) | | | UNCLASSIFIED | 1053 |
| 4878 | 57439464 (3413, 3414) | | | UNCLASSIFIED | 1058 |
| 4879 | 79461401 (3417, 3418) | | | UNCLASSIFIED | 1034 |
| 4880 | 78299175 (3423, 3424) | | | UNCLASSIFIED | 1026 |
| 4881 | 23296404 (3429, 3430) | | | UNCLASSIFIED | 1023 |
| 4882 | 78903906 (3433, 3434) | | | UNCLASSIFIED | 1044 |
| 4883 | 23298372 (3437, 3438) | | | UNCLASSIFIED | 1003, 1016, 1023, 1024, 1039 |
| 4884 | 19741655 (3445, 3446) | | | UNCLASSIFIED | 1003 |
| 4885 | 95011723 (3481, 3482) | | | UNCLASSIFIED | 1006 |
| 4886 | 33188621 (3497, 3498) | | | UNCLASSIFIED | 1026 |
| 4887 | 29359063 (3505, 3506) | | | UNCLASSIFIED | 1022 |
| 4888 | 94319574 (3529, 3530) | | | UNCLASSIFIED | 1010 |
| 4889 | 37031442 (3533, 3534) | | | UNCLASSIFIED | 1038 |
| 4890 | 35992049 (3535, 3536) | | | UNCLASSIFIED | 1030 |
| 4891 | 20730668 (3545, 3546) | | | UNCLASSIFIED | 1006 |
| 4892 | 80079949 (3563, 3564) | | | UNCLASSIFIED | 1034 |

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| 4893 | 16321749 (3587, 3588) | | UNCLASSIFIED | 1004 |
| 4894 | 65706307 (3593, 3594) | | UNCLASSIFIED | 1038 |
| 4895 | 80082839 (3597, 3598) | | UNCLASSIFIED | 1001 |
| 4896 | 28817494 (3611, 3612) | | UNCLASSIFIED | 1017 |
| 4897 | 94139733 (3617, 3618) | | UNCLASSIFIED | 1044 |
| 4898 | 70565738 (3629, 3630) | | UNCLASSIFIED | 1036 |
| 4899 | 18589178 (3643, 3644) | | UNCLASSIFIED | 1001 |
| 4900 | 79460967 (3649, 3650) | | UNCLASSIFIED | 1001 |
| 4901 | 33207465 (3653, 3654) | | UNCLASSIFIED | 1026 |
| 4902 | 56156638 (3671, 3672) | | UNCLASSIFIED | 1008 |
| 4903 | 12817719 (3673, 3674) | | UNCLASSIFIED | 1004 |
| 4904 | 23299970 (3675, 3676) | | UNCLASSIFIED | 1026 |
| 4905 | 20289286 (3689, 3690) | | UNCLASSIFIED | 1010 |
| 4906 | 79623244 (3695, 3696) | | UNCLASSIFIED | 1025 |
| 4907 | 80416739 (3697, 3698) | | UNCLASSIFIED | 1001, 1006, 1010, 1025 |
| 4908 | 37801561 (3711, 3712) | | UNCLASSIFIED | 1012 |
| 4909 | 80503340 (3715, 3716) | | UNCLASSIFIED | 1003, 1012, 1022, 1034, 1039, 1044, 1058 |
| 4910 | 23293220 (3723, 3724) | | UNCLASSIFIED | 1026 |

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| 4911 | 20625040 (3755, 3756) | | UNCLASSIFIED | 1010 |
| 4912 | 66256337 (3757, 3758) | | UNCLASSIFIED | 1016 |
| 4913 | 33763794 (3761, 3762) | | UNCLASSIFIED | 1026 |
| 4914 | 65871999 (3771, 3772) | | UNCLASSIFIED | 1016 |
| 4915 | 35063178 (3781, 3782) | | UNCLASSIFIED | 1050 |
| 4916 | 78460774 (3791, 3792) | | UNCLASSIFIED | 1023 |
| 4917 | 38068620 (3829, 3830) | | UNCLASSIFIED | 1009 |
| 4918 | 29443084 (3831, 3832) | | UNCLASSIFIED | 1022 |
| 4919 | 95092187 (3843, 3844) | | UNCLASSIFIED | 1058 |
| 4920 | 95287606 (3847, 3848) | | UNCLASSIFIED | 1038 |
| 4921 | 18558229 (3849, 3850) | | UNCLASSIFIED | 1001 |
| 4922 | 95295881 (3853, 3854) | | UNCLASSIFIED | 1001, 1006, 1016, 1022, 1031, 1034, 1054 |
| 4923 | 80424759 (3859, 3860) | | UNCLASSIFIED | 1017, 1025 |
| 4924 | 7530006 (3861, 3862) | | UNCLASSIFIED | 1058 |
| 4925 | 77667713 (3869, 3870) | | UNCLASSIFIED | 1024 |
| 4926 | 34386848 (3883, 3884) | | UNCLASSIFIED | 1026 |
| 4927 | 80503349 (3885, 3886) | | UNCLASSIFIED | 1012 |
| 4928 | 56149706 (3887, 3888) | | UNCLASSIFIED | 1003 |

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| 4929 | 32125815 (3891, 3892) | | UNCLASSIFIED | 1006 |
| 4930 | 56152322 (3907, 3908) | | UNCLASSIFIED | 1003 |
| 4931 | 20293364 (3925, 3926) | | UNCLASSIFIED | 1034 |
| 4932 | 56158098 (3929, 3930) | | UNCLASSIFIED | 1046 |
| 4933 | 78723348 (3943, 3944) | | UNCLASSIFIED | 1022, 1026 |
| 4934 | 91010277 (3955, 3956) | | UNCLASSIFIED | 1020 |
| 4935 | 8554745 (3959, 3960) | | UNCLASSIFIED | 1053 |
| 4936 | 79563081 (3963, 3964) | | UNCLASSIFIED | 1001 |
| 4937 | 656658407 (3969, 3970) | | UNCLASSIFIED | 1054 |
| 4938 | 79433671 (4011, 4012) | | UNCLASSIFIED | 1017 |
| 4939 | 65886332 (4015, 4016) | | UNCLASSIFIED | 1054 |
| 4940 | 36920987 (4019, 4020) | | UNCLASSIFIED | 1026 |
| 4941 | 32442464 (4065, 4066) | | UNCLASSIFIED | 1000 |
| 4942 | 65977620 (4075, 4076) | | UNCLASSIFIED | 1054 |
| 4943 | 87899145 (4085, 4086) | | UNCLASSIFIED | 1015 |
| 4944 | 55182619 (4087, 4088) | | UNCLASSIFIED | 1019 |
| 4945 | 95089890 (4093, 4094) | | UNCLASSIFIED | 1044 |
| 4946 | 10092799 (4127, 4128) | | UNCLASSIFIED | 1017 |

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| 4947 | 16023937 (4135, 4136) | | UNCLASSIFIED | 1039 |
| 4948 | 39708546 (4153, 4154) | | UNCLASSIFIED | 1039 |
| 4949 | 20724562 (4157, 4158) | | UNCLASSIFIED | 1006 |
| 4950 | 79167066 (4177, 4178) | | UNCLASSIFIED | 1031 |
| 4951 | 16284579 (4183, 4184) | | UNCLASSIFIED | 1054 |
| 4952 | 54994274 (4185, 4186) | | UNCLASSIFIED | 1029 |
| 4953 | 80205103 (4191, 4192) | | UNCLASSIFIED | 1010, 1024, 1034 |
| 4954 | 20434401 (4201, 4202) | | UNCLASSIFIED | 1004 |
| 4955 | 9533119 (4209, 4210) | | UNCLASSIFIED | 1003 |
| 4956 | 13523038 (4229, 4230) | | UNCLASSIFIED | 1034 |
| 4957 | 94232306 (4231, 4232) | | UNCLASSIFIED | 1054 |
| 4958 | 20724566 (4237, 4238) | | UNCLASSIFIED | 1006 |
| 4959 | 65709209 (4239, 4240) | | UNCLASSIFIED | 1023 |
| 4960 | 87586834 (4245, 4246) | | UNCLASSIFIED | 1003 |
| 4961 | 77651477 (4265, 4266) | | UNCLASSIFIED | 1038 |
| 4962 | 11466067 (4269, 4270) | | UNCLASSIFIED | 1024 |
| 4963 | 99412985 (4273, 4274) | | UNCLASSIFIED | 1003, 1022, 1023, 1025 |
| 4964 | 27982079 (4277, 4278) | | UNCLASSIFIED | 1053 |

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| 4965 | 52563623 (4293, 4294) | | UNCLASSIFIED | 1044 |
| 4966 | 19641476 (4307, 4308) | | UNCLASSIFIED | 1034 |
| 4967 | 78389955 (4313, 4314) | | UNCLASSIFIED | 1019, 1030, 1040, 1041 |
| 4968 | 80081684 (4315, 4316) | | UNCLASSIFIED | 1019, 1022, 1042, 1054 |
| 4969 | 80106006 (4319, 4320) | | UNCLASSIFIED | 1007 |
| 4970 | 79647505 (4327, 4328) | | UNCLASSIFIED | 1017, 1038 |
| 4971 | 9678256 (4329, 4330) | | UNCLASSIFIED | 1044 |
| 4972 | 32691420 (4339, 4340) | | UNCLASSIFIED | 1029 |
| 4973 | 79861716 (4345, 4346) | | UNCLASSIFIED | 1023, 1024, 1044 |
| 4974 | 29345933 (4355, 4356) | | UNCLASSIFIED | 1022 |
| 4975 | 78269395 (4359, 4360) | | UNCLASSIFIED | 1029 |
| 4976 | 20297622 (4373, 4374) | | UNCLASSIFIED | 1034 |
| 4977 | 79631863 (4377, 4378) | | UNCLASSIFIED | 1034 |
| 4978 | 65476799 (4379, 4380) | | UNCLASSIFIED | 1038 |
| 4979 | 39550317 (4383, 4384) | | UNCLASSIFIED | 1039 |
| 4980 | 30521361 (4391, 4392) | | UNCLASSIFIED | 1054 |
| 4981 | 5280402 (4421, 4422) | | UNCLASSIFIED | 1058 |
| 4982 | 65636966 (4423, 4424) | | UNCLASSIFIED | 1038 |

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| 4983 | 78790727 (4463, 4464) | | | UNCLASSIFIED | 1044 |
| 4984 | 57311075 (4477, 4478) | | | UNCLASSIFIED | 1054 |
| 4985 | 80591913 (4481, 4482) | | | UNCLASSIFIED | 1026, 1034, 1058 |
| 4986 | 21426530 (4489, 4490) | | | UNCLASSIFIED | 1022 |
| 4987 | 9860417 (4491, 4492) | | | UNCLASSIFIED | 1008 |
| 4988 | 78407047 (4499, 4500) | | | UNCLASSIFIED | 1024 |
| 4989 | 19518039 (4503, 4504) | | | UNCLASSIFIED | 1003 |
| 4990 | 19894316 (4511, 4512) | | | UNCLASSIFIED | 1022 |
| 4991 | 47652936 (4529, 4530) | | | UNCLASSIFIED | 1029 |
| 4992 | 80025810 (4535, 4536) | | | UNCLASSIFIED | 1006 |
| 4993 | 80092973 (4537, 4538) | | | UNCLASSIFIED | 1006 |
| 4994 | 79889279 (4553, 4554) | | | UNCLASSIFIED | 1017 |
| 4995 | 65674254 (4559, 4560) | | | UNCLASSIFIED | 1016 |
| 4996 | 20632651 (4567, 4568) | | | UNCLASSIFIED | 1024 |
| 4997 | 80384201 (4569, 4570) | | | UNCLASSIFIED | 1029, 1050 |
| 4998 | 11130417 (4603, 4604) | | | UNCLASSIFIED | 1034 |
| 4999 | 20731631 (4613, 4614) | | | UNCLASSIFIED | 1006 |
| 5000 | 54857231 (4615, 4616) | | | UNCLASSIFIED | 1019 |

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| 5001 | 91235214 (4641, 4642) | | UNCLASSIFIED | 1010 |
| 5002 | 29470614 (4645, 4646) | | UNCLASSIFIED | 1026 |
| 5003 | 20375287 (4649, 4650) | | UNCLASSIFIED | 1004 |
| 5004 | 6584179 (4655, 4656) | | UNCLASSIFIED | 1003, 1016 |
| 5005 | 2026800 (4673, 4674) | | UNCLASSIFIED | 1004 |
| 5006 | 11810888 (4681, 4682) | | UNCLASSIFIED | 1022 |
| 5007 | 79963471 (4691, 4692) | | UNCLASSIFIED | 1016, 1038, 1044 |
| 5008 | 29690930 (4699, 4700) | | UNCLASSIFIED | 1024 |
| 5009 | 94137625 (4705, 4706) | | UNCLASSIFIED | 1044 |
| 5010 | 78270787 (4707, 4708) | | UNCLASSIFIED | 1039 |
| 5011 | 78506918 (4719, 4720) | | UNCLASSIFIED | 1030, 1054 |
| 5012 | 78750258 (4733, 4734) | | UNCLASSIFIED | 1023 |
| 5013 | 66138179 (4737, 4738) | | UNCLASSIFIED | 1003, 1024 |
| 5014 | 77664712 (4745, 4746) | | UNCLASSIFIED | 1022 |
| 5015 | 91232572 (4759, 4760) | | UNCLASSIFIED | 1002, 1010, 1024 |
| 5016 | 78056504 (4761, 4762) | | UNCLASSIFIED | 1037 |
| 5017 | 25250283 (4779, 4780) | | UNCLASSIFIED | 1039 |
| 5018 | 71095657 (4787, 4788) | | UNCLASSIFIED | 1029, 1053 |

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| 5019 | 80020416 (4799, 4800) | | | UNCLASSIFIED | 1053 |
| 5020 | 79860962 (4803, 4804) | | | UNCLASSIFIED | 1024, 1038, 1054 |
| 5021 | 28976415 (4813, 4814) | | | UNCLASSIFIED | 1022 |
| 5022 | 66726532 (4815, 4816) | | | UNCLASSIFIED | 1009 |
| 5023 | 16801293 (4819, 4820) | | | UNCLASSIFIED | 1017 |
| 5024 | 27826607 (4827, 4828) | | | UNCLASSIFIED | 1022 |
| 5025 | 66142961 (4831, 4832) | | | UNCLASSIFIED | 1010 |
| 5026 | 11805813 (4833, 4834) | | | UNCLASSIFIED | 1022 |
| 5027 | 19755176 (4841, 4842) | | | UNCLASSIFIED | 1003 |
| 5028 | 80468746 (4847, 4848) | | | UNCLASSIFIED | 1012 |
| 5029 | 787793921 (4853, 4854) | | | UNCLASSIFIED | 1003 |
| 5030 | 78510515 (4869, 4870) | | | UNCLASSIFIED | 1008 |
| 5031 | 30274244 (4873, 4874) | | | UNCLASSIFIED | 1008 |
| 5032 | 38057378 (4879, 4880) | | | UNCLASSIFIED | 1054 |
| 5033 | 78928871 (4891, 4892) | | | UNCLASSIFIED | 1039 |
| 5034 | 78380058 (4897, 4898) | | | UNCLASSIFIED | 1008 |
| 5035 | 36858272 (4911, 4912) | | | UNCLASSIFIED | 1016 |
| 5036 | 29225344 (4913, 4914) | | | UNCLASSIFIED | 1024, 1026 |

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| 5037 | 90939146 (4919, 4920) | | | UNCLASSIFIED | 1020, 1046 |
| 5038 | 80499622 (4923, 4924) | | | UNCLASSIFIED | 1003, 1012, 1017, 1034, 1038, 1039 |
| 5039 | 65481477 (4925, 4926) | | | UNCLASSIFIED | 1001, 1049 |
| 5040 | 57307997 (4935, 4936) | | | UNCLASSIFIED | 1022 |
| 5041 | 39734786 (4943, 4944) | | | UNCLASSIFIED | 1026 |
| 5042 | 9948059 (4953, 4954) | | | UNCLASSIFIED | 1044 |
| 5043 | 66667240 (4957, 4958) | | | UNCLASSIFIED | 1029 |
| 5044 | 78797184 (4965, 4966) | | | UNCLASSIFIED | 1026 |
| 5045 | 11310927 (4983, 4984) | | | UNCLASSIFIED | 1024 |
| 5046 | 65652928 (4987, 4988) | | | UNCLASSIFIED | 1016 |
| 5047 | 78254988 (4989, 4990) | | | UNCLASSIFIED | 1010, 1016, 1058 |
| 5048 | 17898109 (4997, 4998) | | | UNCLASSIFIED | 1044 |
| 5049 | 9287013 (5003, 5004) | | | UNCLASSIFIED | 1008 |
| 5050 | 78769680 (5029, 5030) | | | UNCLASSIFIED | 1022 |
| 5051 | 36507186 (5035, 5036) | | | UNCLASSIFIED | 1026 |
| 5052 | 25134632 (5037, 5038) | | | UNCLASSIFIED | 1003 |
| 5053 | 52471815 (5041, 5042) | | | UNCLASSIFIED | 1036 |
| 5054 | 20289034 (5051, 5052) | | | UNCLASSIFIED | 1034 |

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| 5055 | 20475851 (5063, 5064) | | | UNCLASSIFIED | 1022 |
| 5056 | 14995783 (5065, 5066) | | | UNCLASSIFIED | 1024 |
| 5057 | 6343085 (5073, 5074) | | | UNCLASSIFIED | 1058 |
| 5058 | 25264663 (5077, 5078) | | | UNCLASSIFIED | 1054 |
| 5059 | 27957182 (5081, 5082) | | | UNCLASSIFIED | 1004, 1010, 1024 |
| 5060 | 66396658 (5091, 5092) | | | UNCLASSIFIED | 1008 |
| 5061 | 79399274 (5103, 5104) | | | UNCLASSIFIED | 1024 |
| 5062 | 91230076 (5111, 5112) | | | UNCLASSIFIED | 1020, 1054 |
| 5063 | 20297053 (5147, 5148) | | | UNCLASSIFIED | 1022 |
| 5064 | 29692275 (5155, 5156) | | | UNCLASSIFIED | 1016 |
| 5065 | 20688080 (5157, 5158) | | | UNCLASSIFIED | 1010, 1024 |
| 5066 | 16300448 (5159, 5160) | | | UNCLASSIFIED | 1054 |
| 5067 | 36903066 (5177, 5178) | | | UNCLASSIFIED | 1026 |
| 5068 | 29142136 (5221, 5222) | | | UNCLASSIFIED | 1017 |
| 5069 | 79757361 (5227, 5228) | | | UNCLASSIFIED | 1008 |
| 5070 | 32116280 (5229, 5230) | | | UNCLASSIFIED | 1026 |
| 5071 | 20148258 (5235, 5236) | | | UNCLASSIFIED | 1010 |
| 5072 | 47652772 (5237, 5238) | | | UNCLASSIFIED | 1029 |

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| 5073 | 38923105 (5245, 5246) | | UNCLASSIFIED | 1003, 1004, 1006, 1008, 1016, 1017, 1023, 1024, 1025, 1029, 1034, 1038, 1039, 1044, 1054 |
| 5074 | 80408722 (5253, 5254) | | UNCLASSIFIED | |
| 5075 | 20753337 (5275, 5276) | | UNCLASSIFIED | 1006 |
| 5076 | 65485023 (5291, 5292) | | UNCLASSIFIED | 1009 |
| 5077 | 14973283 (5321, 5322) | | UNCLASSIFIED | 1024 |
| 5078 | 11750568 (5337, 5338) | | UNCLASSIFIED | 1038 |
| 5079 | 80238539 (5339, 5340) | | UNCLASSIFIED | 1009, 1022, 1024 |
| 5080 | 20432749 (5347, 5348) | | UNCLASSIFIED | 1024 |
| 5081 | 15021978 (5361, 5362) | | UNCLASSIFIED | 1001 |
| 5082 | 21416541 (5373, 5374) | | UNCLASSIFIED | 1022 |
| 5083 | 79841764 (5395, 5396) | | UNCLASSIFIED | 1044 |
| 5084 | 79560547 (5405, 5406) | | UNCLASSIFIED | 1001 |
| 5085 | 80056227 (5409, 5410) | | UNCLASSIFIED | 1022 |
| 5086 | 15034786 (5423, 5424) | | UNCLASSIFIED | 1004 |
| 5087 | 27982168 (5425, 5426) | | UNCLASSIFIED | 1006 |
| 5088 | 27829707 (5437, 5438) | | UNCLASSIFIED | 1010, 1022, 1024, 1034 |

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| 5099 | 9869112 (5453, 5454) | | | UNCLASSIFIED | 1008 |
| 5090 | 85524525 (5459, 5460) | | | UNCLASSIFIED | 1038 |
| 5091 | 25147891 (5487, 5488) | | | UNCLASSIFIED | 1026 |
| 5092 | 80079956 (5495, 5496) | | | UNCLASSIFIED | 1034 |
| 5093 | 36840157 (5505, 5506) | | | UNCLASSIFIED | 1054 |
| 5094 | 46895245 (5511, 5512) | | | UNCLASSIFIED | 1040 |
| 5095 | 32275643 (5529, 5530) | | | UNCLASSIFIED | 1029 |
| 5096 | 79852247 (5531, 5532) | | | UNCLASSIFIED | 1017 |
| 5097 | 8488502 (5533, 5534) | | | UNCLASSIFIED | 1024 |
| 5098 | 28996372 (5555, 5556) | | | UNCLASSIFIED | 1008 |
| 5099 | 80582192 (5561, 5562) | | | UNCLASSIFIED | 1003, 1010, 1039 |
| 5100 | 55184282 (5577, 5578) | | | UNCLASSIFIED | 1019 |
| 5101 | 10095562 (5579, 5580) | | | UNCLASSIFIED | 1025 |
| 5102 | 16843283 (5587, 5588) | | | UNCLASSIFIED | 1039 |
| 5103 | 11765993 (5593, 5594) | | | UNCLASSIFIED | 1025 |
| 5104 | 65986561 (5605, 5606) | | | UNCLASSIFIED | 1054 |
| 5105 | 94235040 (5609, 5610) | | | UNCLASSIFIED | 1054 |
| 5106 | 79877515 (5615, 5616) | | | UNCLASSIFIED | 1012, 1034 |

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| 5107 | 71238348 (5633, 5634) | | | UNCLASSIFIED | 1000, 1019 |
| 5108 | 79475917 (5635, 5636) | | | UNCLASSIFIED | 1038 |
| 5109 | 32155939 (5657, 5658) | | | UNCLASSIFIED | 1044 |
| 5110 | 78254622 (5683, 5684) | | | UNCLASSIFIED | 1026 |
| 5111 | 16499916 (5687, 5688) | | | UNCLASSIFIED | 1030 |
| 5112 | 54699298 (5693, 5694) | | | UNCLASSIFIED | 1041 |
| 5113 | 79854084 (5695, 5696) | | | UNCLASSIFIED | 1008, 1044 |
| 5114 | 78753175 (5709, 5710) | | | UNCLASSIFIED | 1003, 1017, 1023, 1039, 1044 |
| 5115 | 79190323 (5715, 5716) | | | UNCLASSIFIED | 1024 |
| 5116 | 80245767 (5727, 5728) | | | UNCLASSIFIED | 1004, 1006, 1010, 1012, 1017, 1022, 1034 |
| 5117 | 11688860 (5737, 5738) | | | UNCLASSIFIED | 1031 |
| 5118 | 29357248 (5763, 5764) | | | UNCLASSIFIED | 1026 |
| 5119 | 78908616 (5765, 5766) | | | UNCLASSIFIED | 1023, 1039 |
| 5120 | 66397455 (5767, 5768) | | | UNCLASSIFIED | 1008 |
| 5121 | 80385633 (5781, 5782) | | | UNCLASSIFIED | 1029 |
| 5122 | 86477086 (5809, 5810) | | | UNCLASSIFIED | 1029 |
| 5123 | 86470542 (5829, 5830) | | | UNCLASSIFIED | 1019, 1026 |
| 5124 | 10343959 (5831, 5832) | | | UNCLASSIFIED | 1038 |

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| 5125 | 80496485 (5835, 5836) | UNCLASSIFIED | 1012 |
| 5126 | 13084299 (5839, 5840) | UNCLASSIFIED | 1024 |
| 5127 | 66436551 (5853, 5854) | UNCLASSIFIED | 1024, 1050 |
| 5128 | 27835807 (5859, 5860) | UNCLASSIFIED | 1010, 1024, 1034 |
| 5129 | 30258690 (5863, 5864) | UNCLASSIFIED | 1044 |
| 5130 | 78303488 (5875, 5876) | UNCLASSIFIED | 1026 |
| 5131 | 79213573 (5893, 5894) | UNCLASSIFIED | 1040, 1054 |
| 5132 | 19847679 (5925, 5926) | UNCLASSIFIED | 1034 |
| 5133 | 79562917 (5927, 5928) | UNCLASSIFIED | 1001 |
| 5134 | 29515957 (5929, 5930) | UNCLASSIFIED | 1026 |
| 5135 | 82309349 (5931, 5932) | UNCLASSIFIED | 1001 |
| 5136 | 29005829 (5939, 5940) | UNCLASSIFIED | 1017 |
| 5137 | 79316662 (5959, 5960) | UNCLASSIFIED | 1053 |
| 5138 | 77802701 (5963, 5964) | UNCLASSIFIED | 1054 |
| 5139 | 91014633 (5971, 5972) | UNCLASSIFIED | 1010 |
| 5140 | 29691078 (5977, 5978) | UNCLASSIFIED | 1001, 1024 |
| 5141 | 20291572 (6005, 6006) | UNCLASSIFIED | 1022 |
| 5142 | 79157906 (6013, 6014) | UNCLASSIFIED | 1006 |

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| 5143 | 79558070 (6015, 6016) | | | UNCLASSIFIED | 1003 |
| 5144 | 32304160 (6021, 6022) | | | UNCLASSIFIED | 1000 |
| 5145 | 30645675 (6023, 6024) | | | UNCLASSIFIED | 1008 |
| 5146 | 86466972 (6025, 6026) | | | UNCLASSIFIED | 1029 |
| 5147 | 28459869 (6029, 6030) | | | UNCLASSIFIED | 1030 |
| 5148 | 57058597 (6031, 6032) | | | UNCLASSIFIED | 1054 |
| 5149 | 10262117 (6037, 6038) | | | UNCLASSIFIED | 1023 |
| 5150 | 95416394 (6039, 6040) | | | UNCLASSIFIED | 1017, 1029, 1058 |
| 5151 | 78029109 (6043, 6044) | | | UNCLASSIFIED | 1026 |
| 5152 | 79633269 (6055, 6056) | | | UNCLASSIFIED | 1038 |
| 5153 | 1693411 (6061, 6062) | | | UNCLASSIFIED | 1039 |
| 5154 | 55187264 (6069, 6070) | | | UNCLASSIFIED | 1019 |
| 5155 | 10358054 (6073, 6074) | | | UNCLASSIFIED | 1039 |
| 5156 | 7839326 (6077, 6078) | | | UNCLASSIFIED | 1030, 1034 |
| 5157 | 4982371 (6083, 6084) | | | UNCLASSIFIED | 1036 |
| 5158 | 37798845 (6107, 6108) | | | UNCLASSIFIED | 1012 |
| 5159 | 17931705 (6123, 6124) | | | UNCLASSIFIED | 1023 |
| 5160 | 8502281 (6129, 6130) | | | UNCLASSIFIED | 1010 |

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| 5161 | 11799333 (6141, 6142) | | UNCLASSIFIED | 1038 |
| 5162 | 79637416 (6147, 6148) | | UNCLASSIFIED | 1044 |
| 5163 | 79581619 (6151, 6152) | | UNCLASSIFIED | 1016, 1040 |
| 5164 | 52229838 (6155, 6156) | | UNCLASSIFIED | 1036 |
| 5165 | 79796272 (6157, 6158) | | UNCLASSIFIED | 1024, 1025, 1044 |
| 5166 | 30537150 (6173, 6174) | | UNCLASSIFIED | 1026 |
| 5167 | 78523718 (6175, 6176) | | UNCLASSIFIED | 1008 |
| 5168 | 88068474 (6177, 6178) | | UNCLASSIFIED | 1053 |
| 5169 | 11130780 (6185, 6186) | | UNCLASSIFIED | 1006 |
| 5170 | 16421170 (6189, 6190) | | UNCLASSIFIED | 1003 |
| 5171 | 20633758 (6193, 6194) | | UNCLASSIFIED | 1004 |
| 5172 | 79846212 (6211, 6212) | | UNCLASSIFIED | 1044 |
| 5173 | 28374356 (6213, 6214) | | UNCLASSIFIED | 1024 |
| 5174 | 98943853 (6215, 6216) | | UNCLASSIFIED | 1010, 1031, 1043 |
| 5175 | 25248469 (6221, 6222) | | UNCLASSIFIED | 1023 |
| 5176 | 80039970 (6225, 6226) | | UNCLASSIFIED | 1022 |
| 5177 | 79610204 (6227, 6228) | | UNCLASSIFIED | 1039 |
| 5178 | 57057121 (6237, 6238) | | UNCLASSIFIED | 1054 |

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| 5179 | 86465890 (6239, 6240) | | | UNCLASSIFIED | 1029 |
| 5180 | 20294907 (6243, 6244) | | | UNCLASSIFIED | 1022 |
| 5181 | 80085241 (6245, 6246) | | | UNCLASSIFIED | 1054 |
| 5182 | 87455587 (6255, 6256) | | | UNCLASSIFIED | 1025 |
| 5183 | 78971204 (6265, 6266) | | | UNCLASSIFIED | 1003 |
| 5184 | 27805779 (6271, 6272) | | | UNCLASSIFIED | 1022 |
| 5185 | 47652261 (6281, 6282) | | | UNCLASSIFIED | 1029 |
| 5186 | 91228201 (6289, 6290) | | | UNCLASSIFIED | 1010 |
| 5187 | 21437311 (6297, 6298) | | | UNCLASSIFIED | 1034 |
| 5188 | 37034503 (6299, 6300) | | | UNCLASSIFIED | 1012 |
| 5189 | 79914983 (6309, 6310) | | | UNCLASSIFIED | 1044 |
| 5190 | 10279756 (6311, 6312) | | | UNCLASSIFIED | 1025 |
| 5191 | 78379792 (6317, 6318) | | | UNCLASSIFIED | 1026 |
| 5192 | 37017019 (6333, 6334) | | | UNCLASSIFIED | 1025 |
| 5193 | 79815629 (6341, 6342) | | | UNCLASSIFIED | 1017, 1039 |
| 5194 | 86379956 (6353, 6354) | | | UNCLASSIFIED | 1053 |
| 5195 | 19479854 (6359, 6360) | | | UNCLASSIFIED | 1038 |
| 5196 | 79587630 (6369, 6370) | | | UNCLASSIFIED | 1006 |

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| 5197 | 49297665 (6379, 6380) | | UNCLASSIFIED | 1010 |
| 5198 | 20465261 (6387, 6388) | | UNCLASSIFIED | 1025 |
| 5199 | 17663280 (6393, 6394) | | UNCLASSIFIED | 1006 |
| 5200 | 20459354 (6403, 6404) | | UNCLASSIFIED | 1029 |
| 5201 | 37011661 (6415, 6416) | | UNCLASSIFIED | 1034 |
| 5202 | 79485207 (6435, 6436) | | UNCLASSIFIED | 1054 |
| 5203 | 78206913 (6455, 6456) | | UNCLASSIFIED | 1054 |
| 5204 | 65881670 (6481, 6482) | | UNCLASSIFIED | 1017, 1023 |
| 5205 | 71758071 (6495, 6496) | | UNCLASSIFIED | 1010 |
| 5206 | 20431621 (6511, 6512) | | UNCLASSIFIED | 1029 |
| 5207 | 80407779 (6513, 6514) | | UNCLASSIFIED | 1040 |
| 5208 | 49128786 (6519, 6520) | | UNCLASSIFIED | 1034 |
| 5209 | 11071847 (6525, 6526) | | UNCLASSIFIED | 1017 |
| 5210 | 78947573 (6527, 6528) | | UNCLASSIFIED | 1009 |
| 5211 | 65691882 (6541, 6542) | | UNCLASSIFIED | 1004 |
| 5212 | 12806274 (6565, 6566) | | UNCLASSIFIED | 1058 |
| 5213 | 80186759 (6575, 6576) | | UNCLASSIFIED | 1024, 1036 |
| 5214 | 77978838 (6581, 6582) | | | |

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| 5215 | 65686186 (6587, 6588) | UNCLASSIFIED | 1024 |
| 5216 | 25317501 (6597, 6598) | UNCLASSIFIED | 1009 |
| 5217 | 2953222 (6601, 6602) | UNCLASSIFIED | 1017 |
| 5218 | 65689283 (6623, 6624) | UNCLASSIFIED | 1016 |
| 5219 | 80025952 (6629, 6630) | UNCLASSIFIED | 1006, 1023, 1024 |
| 5220 | 78885627 (6631, 6632) | UNCLASSIFIED | 1054 |
| 5221 | 28948543 (6645, 6646) | UNCLASSIFIED | 1024 |
| 5222 | 20466053 (6665, 6666) | UNCLASSIFIED | 1010 |
| 5223 | 86686787 (6673, 6674) | UNCLASSIFIED | 1013 |
| 5224 | 81618962 (6691, 6692) | UNCLASSIFIED | 1004, 1029, 1053, 1054 |
| 5225 | 71770376 (6733, 6734) | UNCLASSIFIED | 1003 |
| 5226 | 94317606 (6739, 6740) | UNCLASSIFIED | 1044 |
| 5227 | 71811056 (6741, 6742) | UNCLASSIFIED | 1022, 1054 |
| 5228 | 54860772 (6751, 6752) | UNCLASSIFIED | 1019 |
| 5229 | 16844173 (6757, 6758) | UNCLASSIFIED | 1039 |
| 5230 | 97993351 (6759, 6760) | UNCLASSIFIED | 1003, 1008, 1010, 1017, 1023, 1024, 1025, 1029, 1038, 1044, 1054 |
| 5231 | 79921799 (6769, 6770) | UNCLASSIFIED | 1003 |

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| 5232 | 87459284 (6779, 6780) | | | UNCLASSIFIED | 1019, 1023, 1025 |
| 5233 | 80259500 (6785, 6786) | | | UNCLASSIFIED | 1024 |
| 5234 | 66176310 (6795, 6796) | | | UNCLASSIFIED | 1016 |
| 5235 | 79957388 (6821, 6822) | | | UNCLASSIFIED | 1025 |
| 5236 | 19873311 (6831, 6832) | | | UNCLASSIFIED | 1022 |
| 5237 | 65703727 (6843, 6844) | | | UNCLASSIFIED | 1038 |
| 5238 | 6329184 (6845, 6846) | | | UNCLASSIFIED | 1058 |
| 5239 | 35091694 (6853, 6854) | | | UNCLASSIFIED | 1050 |
| 5240 | 79974494 (6869, 6870) | | | UNCLASSIFIED | 1025 |
| 5241 | 86380275 (6873, 6874) | | | UNCLASSIFIED | 1053 |
| 5242 | 80420196 (6881, 6882) | | | UNCLASSIFIED | 1008, 1016, 1017, 1025, 1054 |
| 5243 | 40389445 (6885, 6886) | | | UNCLASSIFIED | 1037 |
| 5244 | 37032328 (6889, 6890) | | | UNCLASSIFIED | 1038 |
| 5245 | 3371936 (6893, 6894) | | | UNCLASSIFIED | 1012 |
| 5246 | 11415729 (6897, 6898) | | | UNCLASSIFIED | 1017 |
| 5247 | 27241770 (6899, 6900) | | | UNCLASSIFIED | 1023 |
| 5248 | 80084606 (6901, 6902) | | | UNCLASSIFIED | 1001, 1034 |
| 5249 | 10328610 (6927, 6928) | | | UNCLASSIFIED | 1025 |

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| 5250 | 78951028 (6935, 6936) | | | UNCLASSIFIED | 1023, 1054 |
| 5251 | 80090969 (6965, 6966) | | | UNCLASSIFIED | 1049, 1054 |
| 5252 | 47656639 (6969, 6970) | | | UNCLASSIFIED | 1029 |
| 5253 | 78387151 (6971, 6972) | | | UNCLASSIFIED | 1009, 1044 |
| 5254 | 77673816 (6977, 6978) | | | UNCLASSIFIED | 1003 |
| 5255 | 20630336 (6981, 6982) | | | UNCLASSIFIED | 1004 |
| 5256 | 79571979 (6995, 6996) | | | UNCLASSIFIED | 1010, 1017 |
| 5257 | 25139076 (7005, 7006) | | | UNCLASSIFIED | 1003 |
| 5258 | 79446849 (7015, 7016) | | | UNCLASSIFIED | 1022 |
| 5259 | 13076280 (7031, 7032) | | | UNCLASSIFIED | 1027 |
| 5260 | 66037340 (7033, 7034) | | | UNCLASSIFIED | 1021, 1029, 1032, 1035, 1041, 1054 |
| 5261 | 20295126 (7035, 7036) | | | UNCLASSIFIED | 1034 |
| 5262 | 78184009 (7059, 7060) | | | UNCLASSIFIED | 1053 |
| 5263 | 79211075 (7065, 7066) | | | UNCLASSIFIED | 1054 |
| 5264 | 11306931 (7067, 7068) | | | UNCLASSIFIED | 1022 |
| 5265 | 80049785 (7071, 7072) | | | UNCLASSIFIED | 1008, 1023, 1034, 1039 |
| 5266 | 97993359 (7077, 7078) | | | UNCLASSIFIED | 1010, 1017, 1044, 1054 |
| 5267 | 55762455 (7085, 7086) | | | UNCLASSIFIED | 1044 |

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| 5268 | 78052078 (7093, | | | UNCLASSIFIED | 1026 |
| 5269 | 88003628 (7095, | | | UNCLASSIFIED | 1053 |
| 5270 | 9882665 (7105, | | | UNCLASSIFIED | 1008 |
| 5271 | 10887321 (7137, | | | UNCLASSIFIED | 1027 |
| 5272 | 11816423 (7145, | | | UNCLASSIFIED | 1004 |
| 5273 | 56516535 (7149, | | | UNCLASSIFIED | 1019 |
| 5274 | 78297732 (7151, | | | UNCLASSIFIED | 1028 |
| 5275 | 27832512 (7169, | | | UNCLASSIFIED | 1022 |
| 5276 | 79175341 (7185, | | | UNCLASSIFIED | 1027 |
| 5277 | 55166988 (7203, | | | UNCLASSIFIED | 1050 |
| 5278 | 30533340 (7207, | | | UNCLASSIFIED | 1026 |
| 5279 | 8204666 (7237, | | | UNCLASSIFIED | 1004, 1006, 1010, 1016, 1017, 1022, 1024, 1034 |
| | 7238) | | | | |
| 5280 | 37402588 (7245, | | | UNCLASSIFIED | 1022 |
| 5281 | 66255585 (7249, | | | UNCLASSIFIED | 1016 |
| 5282 | 46845180 (7263, | | | UNCLASSIFIED | 1029 |
| 5283 | 16287283 (7265, | | | UNCLASSIFIED | 1024 |
| 5284 | 79915038 (7267, | | | UNCLASSIFIED | 1017 |
| | 7268) | | | | |

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| 5285 | 77582744 (7273, 7274) | | UNCLASSIFIED | 1008 |
| 5286 | 55882230 (7281, 7282) | | UNCLASSIFIED | 1038 |
| 5287 | 65693312 (7283, 7284) | | UNCLASSIFIED | 1038 |
| 5288 | 38439731 (7287, 7288) | | UNCLASSIFIED | 1054 |
| 5289 | 79480190 (7289, 7290) | | UNCLASSIFIED | 1016 |
| 5290 | 30633858 (7309, 7310) | | UNCLASSIFIED | 1026 |
| 5291 | 78676478 (7319, 7320) | | UNCLASSIFIED | 1026 |
| 5292 | 94845520 (7337, 7338) | | UNCLASSIFIED | 1023, 1044 |
| 5293 | 78466294 (7359, 7360) | | UNCLASSIFIED | 1026 |
| 5294 | 29943577 (7369, 7370) | | UNCLASSIFIED | 1044 |
| 5295 | 21415303 (7373, 7374) | | UNCLASSIFIED | 1034 |
| 5296 | 25337090 (7375, 7376) | | UNCLASSIFIED | 1008 |
| 5297 | 79842689 (7409, 7410) | | UNCLASSIFIED | 1008 |
| 5298 | 65981076 (7423, 7424) | | UNCLASSIFIED | 1024 |
| 5299 | 80020956 (7431, 7432) | | UNCLASSIFIED | 1022 |
| 5300 | 9893852 (7437, 7438) | | UNCLASSIFIED | 1039 |
| 5301 | 27981587 (7439, 7440) | | UNCLASSIFIED | 1006 |
| 5302 | 80232031 (7453, 7454) | | UNCLASSIFIED | 1010, 1022, 1034 |

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| 5303 | 80478229 (7455, 7456) | | UNCLASSIFIED | 1012 |
| 5304 | 27958113 (7467, 7468) | | UNCLASSIFIED | 1022 |
| 5305 | 10801357 (7471, 7472) | | UNCLASSIFIED | 1017 |
| 5306 | 79832873 (7477, 7478) | | UNCLASSIFIED | 1023 |
| 5307 | 30198354 (7495, 7496) | | UNCLASSIFIED | 1026 |
| 5308 | 17888333 (7497, 7498) | | UNCLASSIFIED | 1023 |
| 5309 | 25256495 (7505, 7506) | | UNCLASSIFIED | 1026 |
| 5310 | 54540267 (7521, 7522) | | UNCLASSIFIED | 1041 |
| 5311 | 20287238 (7551, 7552) | | UNCLASSIFIED | 1034 |
| 5312 | 80502619 (7553, 7554) | | UNCLASSIFIED | 1004, 1006, 1010, 1012, 1022, 1024, 1027, 1031, 1034 |
| 5313 | 28389124 (7565, 7566) | | UNCLASSIFIED | 1054 |
| 5314 | 27843382 (7567, 7568) | | UNCLASSIFIED | 1022 |
| 5315 | 66390306 (7571, 7572) | | UNCLASSIFIED | 1004, 1006, 1038 |
| 5316 | 7529965 (7575, 7576) | | UNCLASSIFIED | 1058 |
| 5317 | 65881563 (7577, 7578) | | UNCLASSIFIED | 1016 |
| 5318 | 54694326 (7609, 7610) | | UNCLASSIFIED | 1041 |
| 5319 | 11358001 (7631, 7632) | | UNCLASSIFIED | 1058 |

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| 5320 | 32742508 (7653, 7654) | | UNCLASSIFIED | 1012 |
| 5321 | 11769418 (7659, 7660) | | UNCLASSIFIED | 1027 |
| 5322 | 86381109 (7665, 7666) | | UNCLASSIFIED | 1053 |
| 5323 | 79633483 (7669, 7670) | | UNCLASSIFIED | 1016, 1038 |
| 5324 | 85512909 (7675, 7676) | | UNCLASSIFIED | 1053 |
| 5325 | 78771376 (7685, 7686) | | UNCLASSIFIED | 1039 |
| 5326 | 783117247 (7691, 7692) | | UNCLASSIFIED | 1026 |
| 5327 | 11362141 (7695, 7696) | | UNCLASSIFIED | 1024 |
| 5328 | 94672870 (7699, 7700) | | UNCLASSIFIED | 1031, 1034 |
| 5329 | 32739119 (7701, 7702) | | UNCLASSIFIED | 1012 |
| 5330 | 17897290 (7715, 7716) | | UNCLASSIFIED | 1024 |
| 5331 | 21433383 (7717, 7718) | | UNCLASSIFIED | 1022, 1024 |
| 5332 | 65462322 (7719, 7720) | | UNCLASSIFIED | 1054 |
| 5333 | 78373342 (7721, 7722) | | UNCLASSIFIED | 1013 |
| 5334 | 80199079 (7725, 7726) | | UNCLASSIFIED | 1034 |
| 5335 | 80041749 (7731, 7732) | | UNCLASSIFIED | 1022 |
| 5336 | 87454729 (7737, 7738) | | UNCLASSIFIED | 1025 |
| 5337 | 94129384 (7743, 7744) | | UNCLASSIFIED | 1025 |

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| 5338 | 47656514 (7745, 7746) | | | UNCLASSIFIED | 1029, 1053 |
| 5339 | 80078875 (7749, 7750) | | | UNCLASSIFIED | 1001, 1023, 1034, 1054 |
| 5340 | 66173240 (7753, 7754) | | | UNCLASSIFIED | 1016 |
| 5341 | 36831091 (7761, 7762) | | | UNCLASSIFIED | 1054 |
| 5342 | 30173985 (7767, 7768) | | | UNCLASSIFIED | 1016 |
| 5343 | 78781003 (7769, 7770) | | | UNCLASSIFIED | 1026 |
| 5344 | 80451553 (7783, 7784) | | | UNCLASSIFIED | 1017, 1038, 1044 |
| 5345 | 20435513 (7785, 7786) | | | UNCLASSIFIED | 1024 |
| 5346 | 47652570 (7797, 7798) | | | UNCLASSIFIED | 1029 |
| 5347 | 35058689 (7799, 7800) | | | UNCLASSIFIED | 1050 |
| 5348 | 15028582 (7805, 7806) | | | UNCLASSIFIED | 1054 |
| 5349 | 13085170 (7841, 7842) | | | UNCLASSIFIED | 1024 |
| 5350 | 11307308 (7869, 7870) | | | UNCLASSIFIED | 1024 |
| 5351 | 65495369 (7873, 7874) | | | UNCLASSIFIED | 1023 |
| 5352 | 65685027 (7911, 7912) | | | UNCLASSIFIED | 1054 |
| 5353 | 10194093 (7919, 7920) | | | UNCLASSIFIED | 1003 |
| 5354 | 19858661 (7937, 7938) | | | UNCLASSIFIED | 1034 |
| 5355 | 79233133 (7939, 7940) | | | UNCLASSIFIED | 1001 |

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| 5356 | 80034646 (7941, 7942) | | UNCLASSIFIED | 1053 |
| 5357 | 25259664 (7975, 7976) | | UNCLASSIFIED | 1008 |
| 5358 | 77884135 (7981, 7982) | | UNCLASSIFIED | 1021 |
| 5359 | 79193832 (7985, 7986) | | UNCLASSIFIED | 1024 |
| 5360 | 80051547 (7987, 7988) | | UNCLASSIFIED | 1004 |
| 5361 | 35606174 (8007, 8008) | | UNCLASSIFIED | 1053 |
| 5362 | 80200441 (8017, 8018) | | UNCLASSIFIED | 1034 |
| 5363 | 79776383 (8019, 8020) | | UNCLASSIFIED | 1003 |
| 5364 | 33201958 (8031, 8032) | | UNCLASSIFIED | 1026 |
| 5365 | 34270252 (8045, 8046) | | UNCLASSIFIED | 1028 |
| 5366 | 77918724 (8051, 8052) | | UNCLASSIFIED | 1036 |
| 5367 | 65497348 (8057, 8058) | | UNCLASSIFIED | 1016 |
| 5368 | 79249505 (8069, 8070) | | UNCLASSIFIED | 1003, 1038 |
| 5369 | 29676953 (8085, 8086) | | UNCLASSIFIED | 1030 |
| 5370 | 80503197 (8105, 8106) | | UNCLASSIFIED | 1004, 1012, 1034 |
| 5371 | 11602269 (8107, 8108) | | UNCLASSIFIED | 1024 |
| 5372 | 79261068 (8121, 8122) | | UNCLASSIFIED | 1024, 1054 |
| 5373 | 39500183 (8127, 8128) | | UNCLASSIFIED | 1006 |

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| 5374 | 34408232 (8131, 8132) | UNCLASSIFIED | 1030 |
| 5375 | 79474566 (8135, 8136) | UNCLASSIFIED | 1025 |
| 5376 | 34408864 (8139, 8140) | UNCLASSIFIED | 1026 |
| 5377 | 79574372 (8145, 8146) | UNCLASSIFIED | 1010, 1023, 1031, 1049 |
| 5378 | 86670079 (8149, 8150) | UNCLASSIFIED | 1054 |
| 5379 | 17290402 (8157, 8158) | UNCLASSIFIED | 1008 |
| 5380 | 94315126 (8161, 8162) | UNCLASSIFIED | 1020 |
| 5381 | 78707921 (8169, 8170) | UNCLASSIFIED | 1008 |
| 5382 | 78911634 (8179, 8180) | UNCLASSIFIED | 1017, 1037 |
| 5383 | 11765583 (8219, 8220) | UNCLASSIFIED | 1038 |
| 5384 | 20467267 (8239, 8240) | UNCLASSIFIED | 1010 |
| 5385 | 80100236 (8241, 8242) | UNCLASSIFIED | 1004, 1016, 1026 |
| 5386 | 79330843 (8243, 8244) | UNCLASSIFIED | 1022 |
| 5387 | 86689822 (8245, 8246) | UNCLASSIFIED | 1022, 1023 |
| 5388 | 16521538 (8247, 8248) | UNCLASSIFIED | 1003, 1034 |
| 5389 | 65897456 (8265, 8266) | UNCLASSIFIED | 1006, 1016 |
| 5390 | 46849742 (8281, 8282) | UNCLASSIFIED | 1029 |
| 5391 | 11102986 (8283, 8284) | UNCLASSIFIED | 1053 |

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| 5392 | 18545703 (8303, 8304) | | UNCLASSIFIED | 1058 |
| 5393 | 55309111 (8305, 8306) | | UNCLASSIFIED | 1019 |
| 5394 | 79834547 (8309, 8310) | | UNCLASSIFIED | 1008 |
| 5395 | 42723360 (8311, 8312) | | UNCLASSIFIED | 1000 |
| 5396 | 95002700 (8321, 8322) | | UNCLASSIFIED | 1003, 1022 |
| 5397 | 30536440 (8327, 8328) | | UNCLASSIFIED | 1026 |
| 5398 | 70336466 (8329, 8330) | | UNCLASSIFIED | 1034, 1049 |
| 5399 | 79635459 (8331, 8332) | | UNCLASSIFIED | 1008 |
| 5400 | 20595048 (8337, 8338) | | UNCLASSIFIED | 1034 |
| 5401 | 78972888 (8353, 8354) | | UNCLASSIFIED | 1034 |
| 5402 | 94991741 (8359, 8360) | | UNCLASSIFIED | 1004, 1006, 1039 |
| 5403 | 66123463 (8371, 8372) | | UNCLASSIFIED | 1003 |
| 5404 | 19507330 (8391, 8392) | | UNCLASSIFIED | 1044 |
| 5405 | 20287851 (8401, 8402) | | UNCLASSIFIED | 1034 |
| 5406 | 20585009 (8407, 8408) | | UNCLASSIFIED | 1058 |
| 5407 | 17933170 (8417, 8418) | | UNCLASSIFIED | 1008 |
| 5408 | 79617973 (8427, 8428) | | UNCLASSIFIED | 1004 |
| 5409 | 86377020 (8433, 8434) | | UNCLASSIFIED | 1000, 1006, 1016, 1024 |

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| 5410 | 10194277 (8435, 8436), | | | UNCLASSIFIED | 1001 |
| 5411 | 66363898 (8451, 8452), | | | UNCLASSIFIED | 1004 |
| 5412 | 80574192 (8459, 8460) | | | UNCLASSIFIED | 1003, 1058 |
| 5413 | 20478822 (8469, 8470) | | | UNCLASSIFIED | 1022 |
| 5414 | 79191734 (8483, 8484) | | | UNCLASSIFIED | 1034 |
| 5415 | 80035632 (8497, 8498) | | | UNCLASSIFIED | 1010 |
| 5416 | 78928891 (8505, 8506) | | | UNCLASSIFIED | 1017, 1023, 1039 |
| 5417 | 20720192 (8519, 8520) | | | UNCLASSIFIED | 1053 |
| 5418 | 20616476 (8527, 8528) | | | UNCLASSIFIED | 1022 |
| 5419 | 30388369 (8535, 8536) | | | UNCLASSIFIED | 1038 |
| 5420 | 11686751 (8539, 8540) | | | UNCLASSIFIED | 1031 |
| 5421 | 20466876 (8547, 8548) | | | UNCLASSIFIED | 1010 |
| 5422 | 11809277 (8549, 8550) | | | UNCLASSIFIED | 1038 |
| 5423 | 80427709 (8559, 8560) | | | UNCLASSIFIED | 1024, 1025, 1044 |
| 5424 | 78522274 (8595, 8596) | | | UNCLASSIFIED | 1044 |
| 5425 | 20438241 (8613, 8614) | | | UNCLASSIFIED | 1010 |
| 5426 | 35896006 (8623, 8624) | | | UNCLASSIFIED | 1053 |
| 5427 | 33764452 (8625, 8626) | | | UNCLASSIFIED | 1026 |

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| 5428 | 79907203 (8633, 8634), | | | UNCLASSIFIED | 1022, 1038 |
| 5429 | 11809884 (8649, 8650) | | | UNCLASSIFIED | 1016 |
| 5430 | 5980033 (8651, 8652) | | | UNCLASSIFIED | 1058 |
| 5431 | 17707255 (8653, 8654) | | | UNCLASSIFIED | 1008 |
| 5432 | 79564076 (8655, 8656) | | | UNCLASSIFIED | 1017 |
| 5433 | 87452763 (8667, 8668) | | | UNCLASSIFIED | 1008, 1025 |
| 5434 | 80025968 (8675, 8676) | | | UNCLASSIFIED | 1001, 1006, 1017 |
| 5435 | 52493263 (8663, 8684) | | | UNCLASSIFIED | 1036 |
| 5436 | 9398503 (8707, 8708) | | | UNCLASSIFIED | 1017 |
| 5437 | 10299709 (8709, 8710) | | | UNCLASSIFIED | 1038 |
| 5438 | 10868168 (8713, 8714) | | | UNCLASSIFIED | 1034 |
| 5439 | 79872946 (8717, 8718) | | | UNCLASSIFIED | 1001 |
| 5440 | 27842667 (8719, 8720) | | | UNCLASSIFIED | 1004, 1024 |
| 5441 | 30662594 (8721, 8722) | | | UNCLASSIFIED | 1026 |
| 5442 | 30789081 (8725, 8726) | | | UNCLASSIFIED | 1026 |
| 5443 | 46895172 (8753, 8754) | | | UNCLASSIFIED | 1019 |
| 5444 | 9875346 (8779, 8780) | | | UNCLASSIFIED | 1044 |
| 5445 | 30386041 (8785, 8786) | | | UNCLASSIFIED | 1016 |

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| 5446 | 79778177 (8793, 8794) | | | UNCLASSIFIED | 1017 |
| 5447 | 79110241 (8807, 8808) | | | UNCLASSIFIED | 1025 |
| 5448 | 10106140 (6813, 8814) | | | UNCLASSIFIED | 1017 |
| 5449 | 37815429 (8815, 8816) | | | UNCLASSIFIED | 1058 |
| 5450 | 46881608 (8821, 8822) | | | UNCLASSIFIED | 1037 |
| 5451 | 80412188 (8827, 8828) | | | UNCLASSIFIED | 1024, 1029, 1038 |
| 5452 | 19881199 (8831, 8832) | | | UNCLASSIFIED | 1034 |
| 5453 | 30790702 (8833, 8834) | | | UNCLASSIFIED | 1003 |
| 5454 | 65902996 (8849, 8850) | | | UNCLASSIFIED | 1023 |
| 5455 | 78380097 (8861, 8862) | | | UNCLASSIFIED | 1008 |
| 5456 | 56073979 (8869, 8870) | | | UNCLASSIFIED | 1021 |
| 5457 | 65658757 (8875, 8876) | | | UNCLASSIFIED | 1054 |
| 5458 | 16340141 (8877, 8878) | | | UNCLASSIFIED | 1022 |
| 5459 | 79327614 (8909, 8910) | | | UNCLASSIFIED | 1009, 1053 |
| 5460 | 82482238 (8921, 8922) | | | UNCLASSIFIED | 1001, 1008, 1025, 1044 |
| 5461 | 78967938 (8929, 8930) | | | UNCLASSIFIED | 1037, 1038 |
| 5462 | 35107327 (8931, 8932) | | | UNCLASSIFIED | 1030 |
| 5463 | 99102132 (8937, 8938) | | | UNCLASSIFIED | 1006, 1010, 1012, 1023, 1024, 1025, 1054 |

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| 5464 | 79852648 (8939, 8940) | | | UNCLASSIFIED | 1017 |
| 5465 | 86463071 (8943, 8944) | | | UNCLASSIFIED | 1007, 1048 |
| 5466 | 68149385 (8945, 8946) | | | UNCLASSIFIED | 1004 |
| 5467 | 78796432 (8953, 8954) | | | UNCLASSIFIED | 1009 |
| 5468 | 55285269 (8959, 8960) | | | UNCLASSIFIED | 1029, 1053 |
| 5469 | 78386457 (8971, 8972) | | | UNCLASSIFIED | 1003 |
| 5470 | 10173530 (8975, 8976) | | | UNCLASSIFIED | 1039 |
| 5471 | 78160267 (8983, 8984) | | | UNCLASSIFIED | 1024 |
| 5472 | 14160467 (8989, 8990) | | | UNCLASSIFIED | 1053 |
| 5473 | 65888071 (8991, 8992) | | | UNCLASSIFIED | 1054 |
| 5474 | 88078553 (9005, 9006) | | | UNCLASSIFIED | 1008, 1036 |
| 5475 | 65988879 (9017, 9018) | | | UNCLASSIFIED | 1016 |
| 5476 | 54846368 (9033, 9034) | | | UNCLASSIFIED | 1041 |
| 5477 | 27981592 (9039, 9040) | | | UNCLASSIFIED | 1006 |
| 5478 | 11698161 (9051, 9052) | | | UNCLASSIFIED | 1031 |
| 5479 | 38895394 (9053, 9054) | | | UNCLASSIFIED | 1037 |
| 5480 | 19888209 (9059, 9060) | | | UNCLASSIFIED | 1001 |
| 5481 | 77948077 (9081, 9082) | | | UNCLASSIFIED | 1019, 1021, 1041 |

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| 5482 | 9873711 (9095, 9096) | | | UNCLASSIFIED | 1017 |
| 5483 | 10328802 (9105, 9106) | | | UNCLASSIFIED | 1025 |
| 5484 | 19876815 (9129, 9130) | | | UNCLASSIFIED | 1034 |
| 5485 | 25263473 (9141, 9142) | | | UNCLASSIFIED | 1022, 1027 |
| 5486 | 27988240 (9145, 9146) | | | UNCLASSIFIED | 1016 |
| 5487 | 35908087 (9147, 9148) | | | UNCLASSIFIED | 1029 |
| 5488 | 79407666 (9149, 9150) | | | UNCLASSIFIED | 1016 |
| 5489 | 65659192 (9151, 9152) | | | UNCLASSIFIED | 1016 |
| 5490 | 66051947 (9155, 9156) | | | UNCLASSIFIED | 1009, 1049 |
| 5491 | 27998832 (9163, 9164) | | | UNCLASSIFIED | 1039 |
| 5492 | 79410463 (9173, 9174) | | | UNCLASSIFIED | 1022, 1024 |
| 5493 | 77528168 (9183, 9184) | | | UNCLASSIFIED | 1038 |
| 5494 | 12952225 (9213, 9214) | | | UNCLASSIFIED | 1024 |
| 5495 | 80079974 (9221, 9222) | | | UNCLASSIFIED | 1034 |
| 5496 | 86681850 (9225, 9226) | | | UNCLASSIFIED | 1007 |
| 5497 | 78361376 (9235, 9236) | | | UNCLASSIFIED | 1007, 1026 |
| 5498 | 13084470 (9237, 9238) | | | UNCLASSIFIED | 1031 |
| 5499 | 56316660 (9271, 9272) | | | UNCLASSIFIED | 1009 |

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| 5500 | 78743384 (9275, 9276) | | UNCLASSIFIED | 1022 |
| 5501 | 65998476 (9277, 9278) | | UNCLASSIFIED | 1038 |
| 5502 | 35106059 (9297, 9298) | | UNCLASSIFIED | 1026 |
| 5503 | 78793562 (9319, 9320) | | UNCLASSIFIED | 1026 |
| 5504 | 19740303 (9325, 9326) | | UNCLASSIFIED | 1003 |
| 5505 | 27348050 (9327, 9328) | | UNCLASSIFIED | 1026 |
| 5506 | 79555086 (9333, 9334) | | UNCLASSIFIED | 1025 |
| 5507 | 65466547 (9365, 9366) | | UNCLASSIFIED | 1054 |
| 5508 | 86684698 (9385, 9386) | | UNCLASSIFIED | 1029 |
| 5509 | 19524167 (9389, 9390) | | UNCLASSIFIED | 1024 |
| 5510 | 91220456 (9403, 9404) | | UNCLASSIFIED | 1016, 1044 |
| 5511 | 85808289 (9417, 9418) | | UNCLASSIFIED | 1038 |
| 5512 | 65886745 (9427, 9428) | | UNCLASSIFIED | 1016 |
| 5513 | 65706400 (9429, 9430) | | UNCLASSIFIED | 1038 |
| 5514 | 25146194 (9439, 9440) | | UNCLASSIFIED | 1026 |
| 5515 | 80504729 (9445, 9446) | | UNCLASSIFIED | 1012 |
| 5516 | 78043389 (9451, 9452) | | UNCLASSIFIED | 1019, 1024 |
| 5517 | 79844495 (9457, 9458) | | UNCLASSIFIED | 1017 |

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| 5518 | 65891771 (9463, 9464) | UNCLASSIFIED | 1054 |
| 5519 | 9686476 (9493, 9494) | UNCLASSIFIED | 1044 |
| 5520 | 91214067 (9497, 9498) | UNCLASSIFIED | 1004, 1038, 1054 |
| 5521 | 33182707 (9499, 9500) | UNCLASSIFIED | 1026 |
| 5522 | 55774697 (9505, 9506) | UNCLASSIFIED | 1042 |
| 5523 | 79570642 (9515, 9516) | UNCLASSIFIED | 1017 |
| 5524 | 16401672 (9517, 9518) | UNCLASSIFIED | 1003 |
| 5525 | 11802897 (9519, 9520) | UNCLASSIFIED | 1038 |
| 5526 | 78674539 (9525, 9526) | UNCLASSIFIED | 1017 |
| 5527 | 20465812 (9539, 9540) | UNCLASSIFIED | 1010 |
| 5528 | 27845638 (9551, 9552) | UNCLASSIFIED | 1004 |
| 5529 | 79862271 (9563, 9564) | UNCLASSIFIED | 1003 |
| 5530 | 80219133 (9573, 9574) | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1023, 1024, 1029 |
| 5531 | 35065361 (9575, 9576) | UNCLASSIFIED | 1054 |
| 5532 | 56155951 (9583, 9584) | UNCLASSIFIED | 1021 |
| 5533 | 37035315 (9591, 9592) | UNCLASSIFIED | 1012 |
| 5534 | 82053475 (9599, 9600) | UNCLASSIFIED | 1016, 1025 |
| 5535 | 17113146 (9605, 9606) | UNCLASSIFIED | 1030 |

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| 5536 | 8757940 (9613, 9614) | | | UNCLASSIFIED | 1004 |
| 5537 | 28483261 (9619, 9620) | | | UNCLASSIFIED | 1017 |
| 5538 | 78297749 (9635, 9636) | | | UNCLASSIFIED | 1026 |
| 5539 | 17112442 (9639, 9640) | | | UNCLASSIFIED | 1017 |
| 5540 | 79796290 (9663, 9664) | | | UNCLASSIFIED | 1006, 1044 |
| 5541 | 66393096 (9673, 9674) | | | UNCLASSIFIED | 1038 |
| 5542 | 10193406 (9689, 9690) | | | UNCLASSIFIED | 1003, 1034 |
| 5543 | 87112156 (9699, 9700) | | | UNCLASSIFIED | 1018, 1029 |
| 5544 | 10887205 (9703, 9704) | | | UNCLASSIFIED | 1027 |
| 5545 | 8488525 (9711, 9712) | | | UNCLASSIFIED | 1022 |
| 5546 | 28390930 (9729, 9730) | | | UNCLASSIFIED | 1044 |
| 5547 | 56069022 (9733, 9734) | | | UNCLASSIFIED | 1021 |
| 5548 | 11696202 (9743, 9744) | | | UNCLASSIFIED | 1034 |
| 5549 | 94234080 (9747, 9748) | | | UNCLASSIFIED | 1054 |
| 5550 | 23295902 (9763, 9764) | | | UNCLASSIFIED | 1008 |
| 5551 | 20754580 (9771, 9772) | | | UNCLASSIFIED | 1053 |
| 5552 | 79814789 (9781, 9782) | | | UNCLASSIFIED | 1017 |
| 5553 | 79564903 (9785, 9786) | | | UNCLASSIFIED | 1001 |

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| 5554 | 30516871 (9797, 9798) | | | UNCLASSIFIED | 1054 |
| 5555 | 66173108 (9809, 9810) | | | UNCLASSIFIED | 1016 |
| 5556 | 79846238 (9813, 9814) | | | UNCLASSIFIED | 1034 |
| 5557 | 79635469 (9817, 9818) | | | UNCLASSIFIED | 1008 |
| 5558 | 26256306 (9823, 9824) | | | UNCLASSIFIED | 1026 |
| 5559 | 25143575 (9825, 9826) | | | UNCLASSIFIED | 1008 |
| 5560 | 87844752 (9837, 9838) | | | UNCLASSIFIED | 1022, 1026 |
| 5561 | 16790707 (9843, 9844) | | | UNCLASSIFIED | 1044 |
| 5562 | 94146857 (9847, 9848) | | | UNCLASSIFIED | 1003 |
| 5563 | 94148515 (9851, 9852) | | | UNCLASSIFIED | 1003 |
| 5564 | 36668675 (9853, 9854) | | | UNCLASSIFIED | 1053 |
| 5565 | 20283588 (9855, 9856) | | | UNCLASSIFIED | 1022 |
| 5566 | 17956663 (9885, 9886) | | | UNCLASSIFIED | 1023 |
| 5567 | 25316725 (9889, 9890) | | | UNCLASSIFIED | 1008 |
| 5568 | 35055197 (9899, 9900) | | | UNCLASSIFIED | 1054 |
| 5569 | 78362601 (9903, 9904) | | | UNCLASSIFIED | 1003 |
| 5570 | 35137716 (9913, 9914) | | | UNCLASSIFIED | 1050 |
| 5571 | 20296406 (9915, 9916) | | | UNCLASSIFIED | 1022 |

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| 5572 | 56513763 (9925, 9926) | | | UNCLASSIFIED | 1019 |
| 5573 | 65506331 (9931, 9932) | | | UNCLASSIFIED | 1016 |
| 5574 | 79829867 (9943, 9944) | | | UNCLASSIFIED | 1003 |
| 5575 | 20084286 (9959, 9960) | | | UNCLASSIFIED | 1034, 1038 |
| 5576 | 79816963 (9969, 9970) | | | UNCLASSIFIED | 1003, 1039 |
| 5577 | 78784691 (9983, 9984) | | | UNCLASSIFIED | 1008 |
| 6578 | 94986285 (9987, 9988) | | | UNCLASSIFIED | 1006, 1022, 1024, 1039 |
| 5579 | 34118129 (10005, 10006) | | | UNCLASSIFIED | 1000 |
| 5580 | 20750713 (10021, 10022) | | | UNCLASSIFIED | 1022 |
| 5581 | 80232467 (10027, 10028) | | | UNCLASSIFIED | 1022, 1023, 1034, 1044, 1053 |
| 5582 | 46777580 (10029, 10030) | | | UNCLASSIFIED | 1021 |
| 5583 | 11122569 (10045, 10046) | | | UNCLASSIFIED | 1053 |
| 5584 | 86687237 (10053, 10054) | | | UNCLASSIFIED | 1007 |
| 5585 | 57301313 (10075, 10076) | | | UNCLASSIFIED | 1004, 1008, 1022, 1024, 1034 |
| 5586 | 28462264 (10077, 10078) | | | UNCLASSIFIED | 1003 |
| 5587 | 30749180 (10081, 10082) | | | UNCLASSIFIED | 1053 |
| 5588 | 85516018 (10089, 10090) | | | UNCLASSIFIED | 1049 |
| 5589 | 29346656 (10091, 10092) | | | UNCLASSIFIED | 1022 |

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| 5590 | 79610411 (10093, 10094) | | UNCLASSIFIED | 1039 |
| 5591 | 77806491 (10095, 10096) | | UNCLASSIFIED | 1054 |
| 5592 | 25258687 (10101, 10102) | | UNCLASSIFIED | 1008 |
| 5593 | 46781301 (10107, 10108) | | UNCLASSIFIED | 1036 |
| 5594 | 24134290 (10113, 10114) | | UNCLASSIFIED | 1009 |
| 5595 | 79966305 (10115, 10116) | | UNCLASSIFIED | 1003, 1008 |
| 5596 | 12995756 (10123, 10124) | | UNCLASSIFIED | 1031 |
| 5597 | 70760894 (10141, 10142) | | UNCLASSIFIED | 1034 |
| 5598 | 9644485 (10163, 10164) | | UNCLASSIFIED | 1039 |
| 5599 | 10199719 (10171, 10172) | | UNCLASSIFIED | 1004 |
| 5600 | 65860849 (10185, 10186) | | UNCLASSIFIED | 1006, 1044 |
| 5601 | 65694352 (10195, 10196) | | UNCLASSIFIED | 1023 |
| 5602 | 77707056 (10209, 10210) | | UNCLASSIFIED | 1044 |
| 5603 | 87467723 (10213, 10214) | | UNCLASSIFIED | 1018 |
| 5604 | 85816113 (10215, 10216) | | UNCLASSIFIED | 1019 |
| 5605 | 80502186 (10219, 10220) | | UNCLASSIFIED | 1012 |
| 5606 | 91228683 (10231, 10232) | | UNCLASSIFIED | 1010 |
| 5607 | 26260597 (10239, 10240) | | UNCLASSIFIED | 1008 |

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| 5608 | 10279525 (10241, 10242), | | | UNCLASSIFIED | 1038 |
| 5609 | 16309960 (10249, 10250), | | | UNCLASSIFIED | 1054 |
| 5610 | 20630358 (10257, 10258) | | | UNCLASSIFIED | 1004 |
| 5611 | 79391995 (10261, 10262) | | | UNCLASSIFIED | 1006, 1058 |
| 5612 | 80421046 (10263, 10264) | | | UNCLASSIFIED | 1017, 1025 |
| 5613 | 80255237 (10281, 10282) | | | UNCLASSIFIED | 1004, 1039 |
| 5614 | 78386464 (10285, 10286) | | | UNCLASSIFIED | 1008, 1026 |
| 5615 | 789930589 (10299, 10300) | | | UNCLASSIFIED | 1054 |
| 5616 | 30539361 (10305, 10306) | | | UNCLASSIFIED | 1026 |
| 5617 | 789906843 (10307, 10308) | | | UNCLASSIFIED | 1023, 1037 |
| 5618 | 46884297 (10317, 10318) | | | UNCLASSIFIED | 1029 |
| 5619 | 202622916 (10321, 10322) | | | UNCLASSIFIED | 1034 |
| 5620 | 16427755 (10337, 10338) | | | UNCLASSIFIED | 1016 |
| 5621 | 8213493 (10343, 10344) | | | UNCLASSIFIED | 1022 |
| 5622 | 54995422 (10355, 10356) | | | UNCLASSIFIED | 1029 |
| 5623 | 87111945 (10359, 10360) | | | UNCLASSIFIED | 1007 |
| 5624 | 79825759 (10361, 10362) | | | UNCLASSIFIED | 1044 |
| 5625 | 11399291 (10371, 10372) | | | UNCLASSIFIED | 1006 |

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| 5626 | 16311252 (10373, 10374) | | | UNCLASSIFIED | 1054 |
| 5627 | 23289740 (10379, 10380) | | | UNCLASSIFIED | 1039 |
| 5628 | 19726070 (10385, 10386) | | | UNCLASSIFIED | 1001 |
| 5629 | 79769400 (10395, 10396) | | | UNCLASSIFIED | 1023 |
| 5630 | 78393145 (10405, 10406) | | | UNCLASSIFIED | 1038 |
| 5631 | 79187152 (10409, 10410) | | | UNCLASSIFIED | 1024 |
| 5632 | 28480089 (10423, 10424) | | | UNCLASSIFIED | 1008 |
| 5633 | 78307291 (10431, 10432) | | | UNCLASSIFIED | 1010, 1021, 1026, 1042, 1050 |
| 5634 | 94134692 (10439, 10440) | | | UNCLASSIFIED | 1010, 1016, 1023 |
| 5635 | 78296125 (10441, 10442) | | | UNCLASSIFIED | 1026, 1038 |
| 5636 | 7423129 (10443, 10444) | | | UNCLASSIFIED | 1058 |
| 5637 | 36999945 (10449, 10450) | | | UNCLASSIFIED | 1001 |
| 5638 | 94857367 (10453, 10454) | | | UNCLASSIFIED | 1044 |
| 5639 | 28991438 (10459, 10460) | | | UNCLASSIFIED | 1022 |
| 5640 | 20465281 (10473, 10474) | | | UNCLASSIFIED | 1010 |
| 5641 | 19881808 (10475, 10476) | | | UNCLASSIFIED | 1034 |
| 5642 | 25316013 (10479, 10480) | | | UNCLASSIFIED | 1008 |
| 5643 | 35104971 (10505, 10506) | | | UNCLASSIFIED | 1029 |

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| 5644 | 88095343 (10507, 10508) | | UNCLASSIFIED | 1003, 1004, 1006, 1008, 1010, 1012, 1017, 1022, 1026, 1034, 1044 |
| 5645 | 7895594 (10529, 10530) | | UNCLASSIFIED | 1008 |
| 5646 | 46891680 (10531, 10532) | | UNCLASSIFIED | 1019 |
| 5647 | 10090155 (10551, 10552) | | UNCLASSIFIED | 1017 |
| 5648 | 94147972 (10569, 10570) | | UNCLASSIFIED | 1044 |
| 5649 | 65668068 (10579, 10580) | | UNCLASSIFIED | 1053 |
| 5650 | 79471521 (10639, 10640) | | UNCLASSIFIED | 1038 |
| 5651 | 78794326 (10647, 10648) | | UNCLASSIFIED | 1023 |
| 5652 | 28775148 (10659, 10660) | | UNCLASSIFIED | 1017 |
| 5653 | 94134697 (10665, 10666) | | UNCLASSIFIED | 1003 |
| 5654 | 11243179 (10685, 10686) | | UNCLASSIFIED | 1010 |
| 5655 | 37004946 (10689, 10690) | | UNCLASSIFIED | 1029 |
| 5656 | 11122121 (10691, 10692) | | UNCLASSIFIED | 1022 |
| 5657 | 80226630 (10693, 10694) | | UNCLASSIFIED | 1022 |
| 5658 | 32149728 (10695, 10696) | | UNCLASSIFIED | 1029 |
| 5659 | 79441310 (10697, 10698) | | UNCLASSIFIED | 1001, 1016 |
| 5660 | 20432776 (10719, 10720) | | UNCLASSIFIED | 1024 |

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| 5661 | 98951544 (10725, 10726) | | UNCLASSIFIED | 1025, 1038, 1042 |
| 5662 | 94132198 (10735, 10736) | | UNCLASSIFIED | 1003, 1022 |
| 5663 | 78706056 (10747, 10748) | | UNCLASSIFIED | 1025 |
| 5664 | 11707882 (10751, 10752) | | UNCLASSIFIED | 1031 |
| 5665 | 16538333 (10765, 10766) | | UNCLASSIFIED | 1010 |
| 5666 | 28463541 (10773, 10774) | | UNCLASSIFIED | 1024 |
| 5667 | 33207901 (10775, 10776) | | UNCLASSIFIED | 1026 |
| 5668 | 29891912 (10783, 10784) | | UNCLASSIFIED | 1024 |
| 5669 | 78459861 (10807, 10808) | | UNCLASSIFIED | 1026 |
| 5670 | 79617635 (10813, 10814) | | UNCLASSIFIED | 1003 |
| 5671 | 20608797 (10831, 10832) | | UNCLASSIFIED | 1004 |
| 5672 | 85528433 (10843, 10844) | | UNCLASSIFIED | 1016, 1038 |
| 5673 | 79966785 (10847, 10848) | | UNCLASSIFIED | 1003, 1038, 1054 |
| 5674 | 79489975 (10853, 10854) | | UNCLASSIFIED | 1038 |
| 5675 | 79116753 (10869, 10870) | | UNCLASSIFIED | 1013 |
| 5676 | 20287505 (10875, 10876) | | UNCLASSIFIED | 1034 |
| 5677 | 79314110 (10883, 10884) | | UNCLASSIFIED | 1022, 1058 |
| 5678 | 79607120 (10885, 10886) | | UNCLASSIFIED | 1001, 1036, 1050 |

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| 5680 | 37062168 (10889, 10890) | | | UNCLASSIFIED | 1054 |
| 5681 | 65893063 (10899, 10900) | | | UNCLASSIFIED | 1054 |
| 5682 | 94239912 (10907, 10908) | | | UNCLASSIFIED | 1039 |
| 5683 | 46853046 (10909, 10910) | | | UNCLASSIFIED | 1037 |
| 5684 | 78489931 (10915, 10916) | | | UNCLASSIFIED | 1054 |
| 5685 | 20466896 (10923, 10924) | | | UNCLASSIFIED | 1010 |
| 5686 | 85814060 (10939, 10940) | | | UNCLASSIFIED | 1038 |
| 5687 | 30631955 (10943, 10944) | | | UNCLASSIFIED | 1022 |
| 5688 | 65884532 (10949, 10950) | | | UNCLASSIFIED | 1054 |
| 5689 | 17882450 (10969, 10970) | | | UNCLASSIFIED | 1039 |
| 5690 | 78707221 (10971, 10972) | | | UNCLASSIFIED | 1039 |
| 5691 | 30526078 (10979, 10980) | | | UNCLASSIFIED | 1012 |
| 5692 | 28479005 (10981, 10982) | | | UNCLASSIFIED | 1022 |
| 5693 | 16750434 (10991, 10992) | | | UNCLASSIFIED | 1039 |
| 5694 | 77881613 (11007, 11008) | | | UNCLASSIFIED | 1019 |
| 5695 | 85528260 (11017, 11018) | | | UNCLASSIFIED | 1049 |
| 5696 | 34664696 (11019, 11020) | | | UNCLASSIFIED | 1024 |

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| 5697 | 98811078 (11021, 11022) | | | UNCLASSIFIED | 1008, 1010, 1058 |
| 5698 | 17885580 (11023, 11024) | | | UNCLASSIFIED | 1024 |
| 5699 | 78077942 (11025, 11026) | | | UNCLASSIFIED | 1029 |
| 5700 | 46775729 (11027, 11028) | | | UNCLASSIFIED | 1021 |
| 5701 | 55778000 (11043, 11044) | | | UNCLASSIFIED | 1021 |
| 5702 | 85531395 (11045, 11046) | | | UNCLASSIFIED | 1038 |
| 5703 | 11392476 (11049, 11050) | | | UNCLASSIFIED | 1024 |
| 5704 | 65660735 (11077, 11078) | | | UNCLASSIFIED | 1053 |
| 5705 | 91238820 (11083, 11084) | | | UNCLASSIFIED | 1010 |
| 5706 | 57158191 (11085, 11086) | | | UNCLASSIFIED | 1034 |
| 5707 | 78979937 (11087, 11088) | | | UNCLASSIFIED | 1024, 1038 |
| 5708 | 78954675 (11091, 11092) | | | UNCLASSIFIED | 1039 |
| 5709 | 81516220 (11103, 11104) | | | UNCLASSIFIED | 1024, 1034, 1039, 1044, 1054, 1058 |
| 5710 | 21629822 (11105, 11106) | | | UNCLASSIFIED | 1029 |
| 5711 | 9383450 (11111, 11112) | | | UNCLASSIFIED | 1017 |
| 5712 | 80229608 (11113, 11114) | | | UNCLASSIFIED | 1006 |
| 5713 | 78239349 (11119, 11120) | | | UNCLASSIFIED | 1008, 1026 |
| 5714 | 78939376 (11131, 11132) | | | UNCLASSIFIED | 1023 |

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| 5715 | 94713900 (11133, 11134) | | | UNCLASSIFIED | 1010 |
| 5716 | 82356540 (11135, 11136) | | | UNCLASSIFIED | 1001, 1006, 1009, 1010, 1016, 1022, 1023, 1025, 1026, 1027, 1034, 1039, 1044, 1054 |
| 5717 | 81929227 (11137, 11138) | | | UNCLASSIFIED | 1012, 1016, 1022, 1044 |
| 5718 | 66151358 (11149, 11150) | | | UNCLASSIFIED | 1024 |
| 5719 | 79834402 (11161, 11162) | | | UNCLASSIFIED | 1008 |
| 5720 | 10370165 (11185, 11186) | | | UNCLASSIFIED | 1044 |
| 5721 | 11698624 (11215, 11216) | | | UNCLASSIFIED | 1031 |
| 5722 | 29689480 (11225, 11226) | | | UNCLASSIFIED | 1054 |
| 5723 | 78375454 (11239, 11240) | | | UNCLASSIFIED | 1016, 1044, 1056 |
| 5724 | 46782308 (11243, 11244) | | | UNCLASSIFIED | 1036 |
| 5725 | 5601181 (11245, 11246) | | | UNCLASSIFIED | 1058 |
| 5726 | 49511773 (11257, 11258) | | | UNCLASSIFIED | 1036 |
| 5727 | 16711666 (11261, 11262) | | | UNCLASSIFIED | 1044 |
| 5728 | 43989154 (11271, 11272) | | | UNCLASSIFIED | 1022 |
| 5729 | 17523511 (11275, 11276) | | | UNCLASSIFIED | 1003 |
| 5730 | 79843241 (11279, 11280) | | | UNCLASSIFIED | 1044 |

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| 5731 | 98280054 (11287, 11288) | | UNCLASSIFIED | 1026, 1054 |
| 5732 | 11294944 (11297, 11298) | | UNCLASSIFIED | 1022 |
| 5733 | 78674631 (11301, 11302) | | UNCLASSIFIED | 1022 |
| 5734 | 789755613 (11303, 11304) | | UNCLASSIFIED | 1023 |
| 5735 | 20475173 (11313, 11314) | | UNCLASSIFIED | 1034 |
| 5736 | 11814766 (11315, 11316) | | UNCLASSIFIED | 1024 |
| 5737 | 17933825 (11331, 11332) | | UNCLASSIFIED | 1038 |
| 5738 | 78389805 (11337, 11338) | | UNCLASSIFIED | 1008 |
| 5739 | 10047151 (11341, 11342) | | UNCLASSIFIED | 1003 |
| 5740 | 16460451 (11373, 11374) | | UNCLASSIFIED | 1023 |
| 5741 | 52567245 (11375, 11376) | | UNCLASSIFIED | 1017 |
| 5742 | 27972629 (11381, 11382) | | UNCLASSIFIED | 1053 |
| 5743 | 88166396 (11383, 11384) | | UNCLASSIFIED | 1006, 1008, 1023, 1024, 1026, 1034, 1039 |
| 5744 | 99385600 (11393, 11394) | | UNCLASSIFIED | 1017, 1039 |
| 5745 | 79582720 (11395, 11396) | | UNCLASSIFIED | 1027 |
| 5746 | 65900847 (11397, 11398) | | UNCLASSIFIED | 1012, 1023 |
| 5747 | 11293031 (11415, 11416) | | UNCLASSIFIED | 1010 |
| 5748 | 35913706 (11419, 11420) | | UNCLASSIFIED | 1029 |

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| 5749 | 11380635 (11451, 11452) | | | UNCLASSIFIED | 1016 |
| 5750 | 39517795 (11455, 11456) | | | UNCLASSIFIED | 1006 |
| 5751 | 9874851 (11457, 11458) | | | UNCLASSIFIED | 1044 |
| 5752 | 78728822 (11459, 11460) | | | UNCLASSIFIED | 1022 |
| 5753 | 80080839 (11461, 11462) | | | UNCLASSIFIED | 1001, 1034 |
| 5754 | 66395865 (11467, 11468) | | | UNCLASSIFIED | 1009 |
| 5755 | 79558181 (11469, 11470) | | | UNCLASSIFIED | 1038 |
| 5756 | 65898006 (11475, 11476) | | | UNCLASSIFIED | 1054 |
| 5757 | 79621395 (11477, 11478) | | | UNCLASSIFIED | 1003 |
| 5758 | 20292105 (11495, 11496) | | | UNCLASSIFIED | 1034 |
| 5759 | 39466729 (11515, 11516) | | | UNCLASSIFIED | 1004 |
| 5760 | 46863141 (11517, 11518) | | | UNCLASSIFIED | 1050 |
| 5761 | 86379982 (11521, 11522) | | | UNCLASSIFIED | 1053 |
| 5762 | 79632973 (11529, 11530) | | | UNCLASSIFIED | 1038 |
| 5763 | 55299529 (11533, 11534) | | | UNCLASSIFIED | 1029 |
| 5764 | 11090092 (11571, 11572) | | | UNCLASSIFIED | 1006 |
| 5765 | 95200178 (11577, 11578) | | | UNCLASSIFIED | 1025 |
| 5766 | 27967667 (11603, 11604) | | | UNCLASSIFIED | 1053 |

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| 5767 | 80224053 (11611, 11612) | | UNCLASSIFIED | 1026 |
| 5768 | 27362132 (11619, 11620) | | UNCLASSIFIED | 1003, 1008, 1010, 1026 |
| 5769 | 79222407 (11631, 11632) | | UNCLASSIFIED | 1008, 1017 |
| 5770 | 79777614 (11637, 11638) | | UNCLASSIFIED | 1008, 1017 |
| 5771 | 65484453 (11659, 11660) | | UNCLASSIFIED | 1038 |
| 5772 | 19893798 (11663, 11664) | | UNCLASSIFIED | 1034 |
| 5773 | 21414303 (11665, 11666) | | UNCLASSIFIED | 1024 |
| 5774 | 35905367 (11669, 11670) | | UNCLASSIFIED | 1029 |
| 5775 | 46671053 (11673, 11674) | | UNCLASSIFIED | 1022 |
| 5776 | 25254883 (11681, 11682) | | UNCLASSIFIED | 1026 |
| 5777 | 9668350 (11689, 11700) | | UNCLASSIFIED | 1034 |
| 5778 | 94134826 (11701, 11702) | | UNCLASSIFIED | 1010, 1038 |
| 5779 | 79209852 (11713, 11714) | | UNCLASSIFIED | 1054 |
| 5780 | 79810843 (11729, 11730) | | UNCLASSIFIED | 1017, 1054 |
| 5781 | 20432511 (11769, 11770) | | UNCLASSIFIED | 1022 |
| 5782 | 78182358 (11775, 11776) | | UNCLASSIFIED | 1026, 1029, 1040, 1053 |
| 5783 | 9679326 (11781, 11782) | | UNCLASSIFIED | 1044 |
| 5784 | 78962171 (11783, 11784) | | UNCLASSIFIED | 1039 |

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| 5785 | 87466217 (11785, 11786) | | UNCLASSIFIED | 1018 |
| 5786 | 79252239 (11787, 11788) | | UNCLASSIFIED | 1008, 1016, 1024, 1038 |
| 5787 | 56714299 (11799, 11800) | | UNCLASSIFIED | 1016, 1036 |
| 5788 | 91235092 (11803, 11804) | | UNCLASSIFIED | 1010 |
| 5789 | 55005621 (11815, 11816) | | UNCLASSIFIED | 1019 |
| 5790 | 80420019 (11835, 11836) | | UNCLASSIFIED | 1001, 1008, 1017, 1025, 1038, 1044 |
| 5791 | 95199434 (11851, 11852) | | UNCLASSIFIED | 1029 |
| 5792 | 13518686 (11871, 11872) | | UNCLASSIFIED | 1034 |
| 5793 | 94652279 (11879, 11880) | | UNCLASSIFIED | 1006 |
| 5794 | 55929780 (11883, 11884) | | UNCLASSIFIED | 1010 |
| 5795 | 78444786 (11885, 11886) | | UNCLASSIFIED | 1026 |
| 5796 | 80200986 (11893, 11894) | | UNCLASSIFIED | 1022, 1023, 1024 |
| 5797 | 79559331 (11899, 11900) | | UNCLASSIFIED | 1039 |
| 5798 | 8757228 (11917, 11918) | | UNCLASSIFIED | 1004 |
| 5799 | 79441478 (11927, 11928) | | UNCLASSIFIED | 1022 |
| 5800 | 33200862 (11935, 11936) | | UNCLASSIFIED | 1026 |
| 5801 | 80248700 (11949, 11950) | | UNCLASSIFIED | 1006, 1008 |
| 5802 | 65981457 (11957, 11958) | | UNCLASSIFIED | 1024, 1027 |

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| 5803 | 12916245 (11971, 11972), | | UNCLASSIFIED | 1024 |
| 5804 | 77797341 (11987, 11988), | | UNCLASSIFIED | 1051 |
| 5805 | 79810441 (11989, 11990), | | UNCLASSIFIED | 1004, 1008, 1017 |
| 5806 | 10300902 (11993, 11994), | | UNCLASSIFIED | 1001 |
| 5807 | 11685240 (12001, 12002), | | UNCLASSIFIED | 1016 |
| 5808 | 20748452 (12009, 12010), | | UNCLASSIFIED | 1022 |
| 5809 | 78187997 (12011, 12012), | | UNCLASSIFIED | 1029 |
| 5810 | 79584969 (12021, 12022), | | UNCLASSIFIED | 1022 |
| 5811 | 80055035 (12029, 12030), | | UNCLASSIFIED | 1004, 1010, 1012, 1027, 1034 |
| 5812 | 46571939 (12033, 12034), | | UNCLASSIFIED | 1029, 1053 |
| 5813 | 71737235 (12043, 12044), | | UNCLASSIFIED | 1003 |
| 5814 | 29143572 (12045, 12046), | | UNCLASSIFIED | 1017 |
| 5815 | 30247621 (12049, 12050), | | UNCLASSIFIED | 1030 |
| 5816 | 55008916 (12055, 12056), | | UNCLASSIFIED | 1019 |
| 5817 | 29348971 (12077, 12078), | | UNCLASSIFIED | 1022 |
| 5818 | 80547299 (12101, 12102), | | UNCLASSIFIED | 1016, 1023, 1024, 1058 |
| 5819 | 32287381 (12109, 12110), | | UNCLASSIFIED | 1029 |
| 5820 | 86473933 (12131, 12132), | | UNCLASSIFIED | 1054 |

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| 5822 | 65668721 (12135, 12136) | UNCLASSIFIED | 1016 |
| 5823 | 11809291 (12145, 12146) | UNCLASSIFIED | 1038 |
| 5824 | 20435968 (12155, 12156) | UNCLASSIFIED | 1024 |
| 5825 | 13086232 (12169, 12170) | UNCLASSIFIED | 1024 |
| 5826 | 79973785 (12189, 12190) | UNCLASSIFIED | 1023 |
| 5827 | 21422499 (12197, 12198) | UNCLASSIFIED | 1004 |
| 5828 | 19514022 (12207, 12208) | UNCLASSIFIED | 1022 |
| 5829 | 20632844 (12213, 12214) | UNCLASSIFIED | 1004 |
| 5830 | 78467254 (12239, 12240) | UNCLASSIFIED | 1008, 1026 |
| 5831 | 34129023 (12263, 12264) | UNCLASSIFIED | 1026 |
| 5832 | 47656539 (12267, 12268) | UNCLASSIFIED | 1029 |
| 5833 | 78254650 (12269, 12270) | UNCLASSIFIED | 1026 |
| 5834 | 27978283 (12271, 12272) | UNCLASSIFIED | 1022 |
| 5835 | 20727944 (12281, 12282) | UNCLASSIFIED | 1006 |
| 5836 | 99413052 (12285, 12286) | UNCLASSIFIED | 1001, 1008, 1010, 1017, 1023, 1037, 1044, 1054 |
| 5837 | 35906642 (12329, 12330) | UNCLASSIFIED | 1029 |

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| 5838 | 79633207 (12363, 12364) | | UNCLASSIFIED | 1039 |
| 5839 | 79828750 (12365, 12366) | | UNCLASSIFIED | 1039 |
| 5840 | 81774665 (12367, 12368) | | UNCLASSIFIED | 1008, 1016, 1023, 1025, 1029, 1034, 1054, 1058 |
| 5841 | 30538258 (12369, 12370) | | UNCLASSIFIED | 1016 |
| 5842 | 79211640 (12371, 12372) | | UNCLASSIFIED | 1054 |
| 5843 | 79866572 (12387, 12388) | | UNCLASSIFIED | 1038 |
| 5844 | 23297387 (12409, 12410) | | UNCLASSIFIED | 1008 |
| 5845 | 80089874 (12413, 12414) | | UNCLASSIFIED | 1010, 1016, 1054 |
| 5846 | 79159603 (12427, 12428) | | UNCLASSIFIED | 1004, 1009, 1022, 1026, 1039, 1053 |
| 5847 | 24133265 (12443, 12444) | | UNCLASSIFIED | 1003 |
| 5848 | 11758131 (12459, 12460) | | UNCLASSIFIED | 1025 |
| 5849 | 80079014 (12475, 12476) | | UNCLASSIFIED | 1034 |
| 5850 | 78381206 (12495, 12496) | | UNCLASSIFIED | 1039 |
| 5851 | 94133459 (12503, 12504) | | UNCLASSIFIED | 1022, 1045 |
| 5852 | 66313988 (12521, 12522) | | UNCLASSIFIED | 1016, 1054 |
| 5853 | 79420151 (12523, 12524) | | UNCLASSIFIED | 1024 |
| 5854 | 28348581 (12529, 12530) | | UNCLASSIFIED | 1024 |

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| 5873 | 29357185 (12731, 12732) | UNCLASSIFIED | 1026 |
| 5874 | 20622170 (12759, 12760) | UNCLASSIFIED | 1004 |
| 5875 | 19539786 (12775, 12776) | UNCLASSIFIED | 1003 |
| 5876 | 65475251 (12787, 12788) | UNCLASSIFIED | 1038 |
| 5877 | 65469684 (12801, 12802) | UNCLASSIFIED | 1038 |
| 5878 | 78408108 (12821, 12822) | UNCLASSIFIED | 1024 |
| 5879 | 11760547 (12829, 12830) | UNCLASSIFIED | 1038 |
| 5880 | 32311406 (12853, 12854) | UNCLASSIFIED | 1029 |
| 5881 | 78767260 (12863, 12864) | UNCLASSIFIED | 1030 |
| 5882 | 87463992 (12869, 12870) | UNCLASSIFIED | 1018 |
| 5883 | 9874073 (12873, 12874) | UNCLASSIFIED | 1044 |
| 5884 | 78955204 (12877, 12878) | UNCLASSIFIED | 1017 |
| 5885 | 8499775 (12879, 12880) | UNCLASSIFIED | 1022 |
| 5886 | 13076808 (12891, 12892) | UNCLASSIFIED | 1022 |
| 5887 | 85547794 (12899, 12900) | UNCLASSIFIED | 1054 |
| 5888 | 29015543 (12903, 12904) | UNCLASSIFIED | 1039 |
| 5889 | 46666410 (12905, 12906) | UNCLASSIFIED | 1022 |
| 5890 | 86679917 (12911, 12912) | UNCLASSIFIED | 1007 |

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| 5891 | 94312044 (12931, 12932) | | UNCLASSIFIED | 1023, 1035 |
| 5892 | 17937413 (12933, 12934) | | UNCLASSIFIED | 1039 |
| 5893 | 30646264 (12935, 12936) | | UNCLASSIFIED | 1008 |
| 5894 | 79241532 (12945, 12946) | | UNCLASSIFIED | 1003, 1016, 1017, 1023, 1024, 1038, 1039, 1044 |
| 5895 | 21149067 (12951, 12952) | | UNCLASSIFIED | 1058 |
| 5896 | 65874895 (12957, 12958) | | UNCLASSIFIED | 1054 |
| 5897 | 5823647 (12963, 12964) | | UNCLASSIFIED | 1058 |
| 5898 | 79836111 (12981, 12982) | | UNCLASSIFIED | 1044 |
| 5899 | 20459851 (12983, 12984) | | UNCLASSIFIED | 1024 |
| 5900 | 79842912 (12985, 12986) | | UNCLASSIFIED | 1004, 1008, 1044 |
| 5901 | 94121682 (13031, 13032) | | UNCLASSIFIED | 1054 |
| 5902 | 79777270 (13043, 13044) | | UNCLASSIFIED | 1017 |
| 5903 | 33765065 (13045, 13046) | | UNCLASSIFIED | 1026 |
| 5904 | 94655391 (13049, 13050) | | UNCLASSIFIED | 1001, 1006, 1008, 1010, 1024, 1034, 1039, 1058 |
| 5905 | 35100519 (13067, 13068) | | UNCLASSIFIED | 1024 |
| 5906 | 24120097 (13071, 13072) | | UNCLASSIFIED | 1026 |

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| 5907 | 10370184 (13075, 13076) | | | UNCLASSIFIED | 1044 |
| 5908 | 87128876 (13093, 13094) | | | UNCLASSIFIED | 1007, 1013, 1016, 1025, 1029, 1034, 1044, 1048 |
| 5909 | 77797987 (13113, 13114) | | | UNCLASSIFIED | 1054 |
| 5910 | 65490646 (13137, 13138) | | | UNCLASSIFIED | 1023 |
| 5911 | 65468664 (13141, 13142) | | | UNCLASSIFIED | 1054 |
| 5912 | 37013642 (13151, 13152) | | | UNCLASSIFIED | 1029 |
| 5913 | 78978053 (13163, 13164) | | | UNCLASSIFIED | 1054 |
| 5914 | 25327049 (13175, 13176) | | | UNCLASSIFIED | 1003 |
| 5915 | 78708986 (13177, 13178) | | | UNCLASSIFIED | 1003 |
| 5916 | 80060983 (13179, 13180) | | | UNCLASSIFIED | 1024, 1039 |
| 5917 | 16549443 (13187, 13188) | | | UNCLASSIFIED | 1003 |
| 5918 | 79914604 (13225, 13226) | | | UNCLASSIFIED | 1006, 1024, 1025 |
| 5919 | 20729402 (13235, 13236) | | | UNCLASSIFIED | 1006 |
| 5920 | 66396359 (13251, 13252) | | | UNCLASSIFIED | 1008 |
| 5921 | 35933698 (13253, 13254) | | | UNCLASSIFIED | 1053 |
| 5922 | 78513264 (13257, 13258) | | | UNCLASSIFIED | 1030 |
| 5923 | 78087821 (13273, 13274) | | | UNCLASSIFIED | 1050 |

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| 5924 | 57306249 (13283, 13284) | | | UNCLASSIFIED | 1003, 1004, 1006, 1009, 1010, 1022, 1023, 1024, 1034, 1039 |
| 5925 | 79865642 (13285, 13286) | | | UNCLASSIFIED | 1017 |
| 5926 | 65896592 (13289, 13290) | | | UNCLASSIFIED | 1038, 1054 |
| 5927 | 36746287 (13293, 13294) | | | UNCLASSIFIED | 1034 |
| 5928 | 19641216 (13305, 13306) | | | UNCLASSIFIED | 1022 |
| 5929 | 79238311 (13313, 13314) | | | UNCLASSIFIED | 1008 |
| 5930 | 32305008 (13335, 13336) | | | UNCLASSIFIED | 1001 |
| 5931 | 79876183 (13339, 13340) | | | UNCLASSIFIED | 1017 |
| 5932 | 36624062 (13345, 13346) | | | UNCLASSIFIED | 1034 |
| 5933 | 65897823 (13347, 13348) | | | UNCLASSIFIED | 1054 |
| 5934 | 79810858 (13359, 13360) | | | UNCLASSIFIED | 1017 |
| 5935 | 33200150 (13365, 13366) | | | UNCLASSIFIED | 1050 |
| 5936 | 30254615 (13369, 13370) | | | UNCLASSIFIED | 1026 |
| 5937 | 32679569 (13371, 13372) | | | UNCLASSIFIED | 1012 |
| 5938 | 79265479 (13377, 13378) | | | UNCLASSIFIED | 1013 |
| 5939 | 11769693 (13387, 13388) | | | UNCLASSIFIED | 1038 |
| 5940 | 51219685 (13395, 13396) | | | UNCLASSIFIED | 1036 |

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| 5941 | 77659114 (13399, 13400) | | | UNCLASSIFIED | 1054 |
| 5942 | 24129461 (13407, 13408) | | | UNCLASSIFIED | 1003 |
| 5943 | 56329354 (13429, 13430) | | | UNCLASSIFIED | 1030 |
| 5944 | 10278706 (13435, 13436) | | | UNCLASSIFIED | 1025 |
| 5945 | 65866244 (13437, 13438) | | | UNCLASSIFIED | 1016 |
| 5946 | 80062425 (13441, 13442) | | | UNCLASSIFIED | 1010 |
| 5947 | 66694286 (13447, 13448) | | | UNCLASSIFIED | 1009 |
| 5948 | 66397495 (13463, 13464) | | | UNCLASSIFIED | 1008, 1030 |
| 5949 | 80027645 (13475, 13476) | | | UNCLASSIFIED | 1006 |
| 5950 | 55769575 (13489, 13490) | | | UNCLASSIFIED | 1038 |
| 5951 | 77474508 (13491, 13492) | | | UNCLASSIFIED | 1023 |
| 5952 | 94255974 (13499, 13500) | | | UNCLASSIFIED | 1008 |
| 5953 | 82205191 (13509, 13510) | | | UNCLASSIFIED | 1004, 1006, 1009, 1016, 1022, 1034 |
| 5954 | 78680880 (13537, 13538) | | | UNCLASSIFIED | 1009, 1022 |
| 5955 | 81793888 (13547, 13548) | | | UNCLASSIFIED | 1010, 1023, 1038, 1044, 1054 |
| 5956 | 54994478 (13551, 13552) | | | UNCLASSIFIED | 1029 |
| 5957 | 86476573 (13559, 13560) | | | UNCLASSIFIED | 1029 |
| 5958 | 79627829 (13575, 13576) | | | UNCLASSIFIED | 1039 |

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| 5959 | 6329693 (13585, 13586) | | | UNCLASSIFIED | 1058 |
| 5960 | 60079026 (13591, 13592) | | | UNCLASSIFIED | 1034 |
| 5961 | 86477481 (13593, 13594) | | | UNCLASSIFIED | 1029 |
| 5962 | 79640376 (13599, 13600) | | | UNCLASSIFIED | 1025 |
| 5963 | 87899013 (13605, 13606) | | | UNCLASSIFIED | 1015 |
| 5964 | 71837603 (13619, 13620) | | | UNCLASSIFIED | 1016, 1030 |
| 5965 | 32339114 (13633, 13634) | | | UNCLASSIFIED | 1029 |
| 5966 | 20262354 (13635, 13636) | | | UNCLASSIFIED | 1034 |
| 5967 | 65902508 (13643, 13644) | | | UNCLASSIFIED | 1010 |
| 5968 | 88096986 (13651, 13652) | | | UNCLASSIFIED | 1025 |
| 5969 | 20286074 (13663, 13664) | | | UNCLASSIFIED | 1022 |
| 5970 | 20484824 (13679, 13680) | | | UNCLASSIFIED | 1022 |
| 5971 | 80056066 (13681, 13682) | | | UNCLASSIFIED | 1022 |
| 5972 | 50104079 (13689, 13690) | | | UNCLASSIFIED | 1036 |
| 5973 | 52211502 (13697, 13698) | | | UNCLASSIFIED | 1036 |
| 5974 | 11814410 (13701, 13702) | | | UNCLASSIFIED | 1006 |
| 5975 | 19517954 (13719, 13720) | | | UNCLASSIFIED | 1003 |
| 5976 | 52382453 (13731, 13732) | | | UNCLASSIFIED | 1036 |

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| 5977 | 91237050 (13735, 13736) | UNCLASSIFIED | 1030 |
| 5978 | 30169544 (13743, 13744) | UNCLASSIFIED | 1054 |
| 5979 | 38439143 (13745, 13746) | UNCLASSIFIED | 1017, 1039 |
| 5980 | 28787444 (13747, 13748) | UNCLASSIFIED | |
| 5981 | 95103762 (13765, 13766) | UNCLASSIFIED | 1003 |
| 5982 | 27966169 (13769, 13770) | UNCLASSIFIED | 1006 |
| 5983 | 79816745 (13777, 13778) | UNCLASSIFIED | 1003 |
| 5984 | 78375927 (13779, 13780) | UNCLASSIFIED | 1004, 1008, 1026 |
| 5985 | 24135857 (13789, 13790) | UNCLASSIFIED | 1003 |
| 5986 | 25336368 (13793, 13794) | UNCLASSIFIED | 1003 |
| 5987 | 38865169 (13795, 13796) | UNCLASSIFIED | 1044 |
| 5988 | 35129892 (13801, 13802) | UNCLASSIFIED | 1012 |
| 5989 | 80155853 (13807, 13808) | UNCLASSIFIED | 1042, 1058 |
| 5990 | 49613350 (13811, 13812) | UNCLASSIFIED | 1036 |
| 5991 | 25341206 (13815, 13816) | UNCLASSIFIED | 1003 |
| 5992 | 65861983 (13845, 13846) | UNCLASSIFIED | 1038 |
| 5993 | 13518036 (13849, 13850) | UNCLASSIFIED | 1024 |
| 5994 | 9277094 (13863, 13864) | UNCLASSIFIED | 1004 |

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| 5995 | 27957397 (13869, 13870) | UNCLASSIFIED | 1022 |
| 5996 | 80499320 (13871, 13872) | UNCLASSIFIED | 1012, 1027 |
| 5997 | 16295194 (13875, 13876) | UNCLASSIFIED | 1054 |
| 5998 | 11813881 (13877, 13878) | UNCLASSIFIED | 1006 |
| 5999 | 55307132 (13905, 13906) | UNCLASSIFIED | 1019 |
| 6000 | 79779635 (13907, 13908) | UNCLASSIFIED | 1003, 1008 |
| 6001 | 91213830 (13917, 13918) | UNCLASSIFIED | 1024 |
| 6002 | 10248646 (13927, 13928) | UNCLASSIFIED | 1038 |
| 6003 | 37009841 (13941, 13942) | UNCLASSIFIED | 1029 |
| 6004 | 49103404 (13951, 13952) | UNCLASSIFIED | 1040 |
| 6005 | 78676716 (13981, 13982) | UNCLASSIFIED | 1009 |
| 6006 | 7920215 (13987, 13988) | UNCLASSIFIED | 1054 |
| 6007 | 80073366 (13999, 14000) | UNCLASSIFIED | 1012, 1024, 1031 |
| 6008 | 20465557 (14011, 14012) | UNCLASSIFIED | 1010 |
| 6009 | 57299429 (14013, 14014) | UNCLASSIFIED | 1003, 1004, 1016, 1022, 1023, 1024, 1026, 1034, 1038 |
| 6010 | 20718836 (14023, 14024) | UNCLASSIFIED | 1053 |
| 6011 | 52222443 (14025, 14026) | UNCLASSIFIED | 1036 |

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| 6012 | 78920547 (14027, 14028) | | | UNCLASSIFIED | 1039 |
| 6013 | 77813198 (14035, 14036) | | | UNCLASSIFIED | 1054 |
| 6014 | 56301392 (14049, 14050) | | | UNCLASSIFIED | 1024 |
| 6015 | 19752312 (14055, 14056) | | | UNCLASSIFIED | 1016 |
| 6016 | 20706304 (14091, 14092) | | | UNCLASSIFIED | 1024 |
| 6017 | 85516704 (14093, 14094) | | | UNCLASSIFIED | 1003, 1004, 1017, 1023, 1053 |
| 6018 | 78315829 (14097, 14098) | | | UNCLASSIFIED | 1026 |
| 6019 | 78765320 (14099, 14100) | | | UNCLASSIFIED | 1008, 1044 |
| 6020 | 20736168 (14109, 14110) | | | UNCLASSIFIED | 1034 |
| 6021 | 65671409 (14113, 14114) | | | UNCLASSIFIED | 1016 |
| 6022 | 66408222 (14121, 14122) | | | UNCLASSIFIED | 1034 |
| 6023 | 94684857 (14123, 14124) | | | UNCLASSIFIED | 1027 |
| 6024 | 86675501 (14125, 14126) | | | UNCLASSIFIED | 1007 |
| 6025 | 35906837 (14127, 14128) | | | UNCLASSIFIED | 1026 |
| 6026 | 13522469 (14147, 14148) | | | UNCLASSIFIED | 1006 |
| 6027 | 34129275 (14155, 14156) | | | UNCLASSIFIED | 1026 |
| 6028 | 19543561 (14169, 14170) | | | UNCLASSIFIED | 1017 |
| 6029 | 81815041 (14175, 14176) | | | UNCLASSIFIED | 1009, 1012, 1016, 1024, 1038, 1054 |

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| 6030 | 19635848 (14183, 14184) | | UNCLASSIFIED | 1006 |
| 6031 | 80059447 (14189, 14190) | | UNCLASSIFIED | 1024, 1034 |
| 6032 | 16414278 (14199, 14200) | | UNCLASSIFIED | 1038 |
| 6033 | 65467837 (14207, 14208) | | UNCLASSIFIED | 1054 |
| 6034 | 80250186 (14211, 14212) | | UNCLASSIFIED | 1022 |
| 6035 | 49602900 (14227, 14228) | | UNCLASSIFIED | 1036 |
| 6036 | 79590636 (14231, 14232) | | UNCLASSIFIED | 1003 |
| 6037 | 82062092 (14239, 14240) | | UNCLASSIFIED | 1012, 1016, 1022, 1023, 1031, 1049 |
| 6038 | 12986531 (14243, 14244) | | UNCLASSIFIED | 1004, 1023 |
| 6039 | 46866687 (14251, 14252) | | UNCLASSIFIED | 1037 |
| 6040 | 10264847 (14253, 14254) | | UNCLASSIFIED | 1038 |
| 6041 | 29227645 (14271, 14272) | | UNCLASSIFIED | 1030 |
| 6042 | 47652463 (14299, 14300) | | UNCLASSIFIED | 1029 |
| 6043 | 13033747 (14301, 14302) | | UNCLASSIFIED | 1027 |
| 6044 | 80254247 (14313, 14314) | | UNCLASSIFIED | 1001, 1004, 1006, 1008, 1010, 1017, 1024, 1038 |
| 6045 | 23286010 (14317, 14318) | | UNCLASSIFIED | 1003 |
| 6046 | 71770118 (14329, 14330) | | UNCLASSIFIED | 1008, 1035 |

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| 6047 | 68990162 (14353, 14354) | | UNCLASSIFIED | 1009 |
| 6048 | 19900534 (14373, 14374) | | UNCLASSIFIED | 1054 |
| 6049 | 80025241 (14379, 14380) | | UNCLASSIFIED | 1004, 1008, 1025, 1026, 1027, 1031, 1034, 1039, 1044 |
| 6050 | 32445289 (14385, 14386) | | UNCLASSIFIED | 1029 |
| 6051 | 10359744 (14397, 14398) | | UNCLASSIFIED | 1039 |
| 6052 | 80251415 (14411, 14412) | | UNCLASSIFIED | 1010 |
| 6053 | 78976740 (14425, 14426) | | UNCLASSIFIED | 1017 |
| 6054 | 77582797 (14429, 14430) | | UNCLASSIFIED | 1008 |
| 6055 | 34406413 (14441, 14442) | | UNCLASSIFIED | 1030 |
| 6056 | 78510094 (14453, 14454) | | UNCLASSIFIED | 1029 |
| 6057 | 78748347 (14459, 14460) | | UNCLASSIFIED | 1026 |
| 6058 | 11818389 (14487, 14488) | | UNCLASSIFIED | 1006 |
| 6059 | 49511790 (14505, 14506) | | UNCLASSIFIED | 1036 |
| 6060 | 55003320 (14509, 14510) | | UNCLASSIFIED | 1019 |
| 6061 | 10370566 (14511, 14512) | | UNCLASSIFIED | 1017 |
| 6062 | 20227865 (14523, 14524) | | UNCLASSIFIED | 1022 |
| 6063 | 86467849 (14537, 14538) | | UNCLASSIFIED | 1019 |

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| 6064 | 86469895 (14551, 14552) | | UNCLASSIFIED | 1029 |
| 6065 | 9863062 (14569, 14570) | | UNCLASSIFIED | 1008 |
| 6066 | 79834203 (14573, 14574) | | UNCLASSIFIED | 1008 |
| 6067 | 80408523 (14575, 14576) | | UNCLASSIFIED | 1006, 1029 |
| 6068 | 65451147 (14583, 14584) | | UNCLASSIFIED | 1016 |
| 6069 | 8500737 (14589, 14590) | | UNCLASSIFIED | 1024 |
| 6070 | 38912306 (14605, 14606) | | UNCLASSIFIED | 1008 |
| 6071 | 30230437 (14611, 14612) | | UNCLASSIFIED | 1026 |
| 6072 | 46685659 (14627, 14628) | | UNCLASSIFIED | 1034 |
| 6073 | 33184195 (14631, 14632) | | UNCLASSIFIED | 1026 |
| 6074 | 66432083 (14643, 14644) | | UNCLASSIFIED | 1024 |
| 6075 | 11763476 (14645, 14646) | | UNCLASSIFIED | 1038 |
| 6076 | 80089891 (14649, 14650) | | UNCLASSIFIED | 1024 |
| 6077 | 55663447 (14653, 14654) | | UNCLASSIFIED | 1021 |
| 6078 | 19726370 (14659, 14660) | | UNCLASSIFIED | 1038 |
| 6079 | 32728850 (14677, 14678) | | UNCLASSIFIED | 1001 |
| 6080 | 55402487 (14709, 14710) | | UNCLASSIFIED | 1019 |
| 6081 | 35910050 (14711, 14712) | | UNCLASSIFIED | 1029 |

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| 6082 | 79642463 (14723, 14724) | UNCLASSIFIED | 1003 |
| 6083 | 65892580 (14727, 14728) | UNCLASSIFIED | 1016 |
| 6084 | 79556093 (14731, 14732) | UNCLASSIFIED | 1003 |
| 6085 | 33763101 (14735, 14736) | UNCLASSIFIED | 1026 |
| 6086 | 79822991 (14751, 14752) | UNCLASSIFIED | 1039 |
| 6087 | 21412199 (14759, 14760) | UNCLASSIFIED | 1034 |
| 6088 | 39524195 (14771, 14772) | UNCLASSIFIED | 1024 |
| 6089 | 95088346 (14777, 14778) | UNCLASSIFIED | 1010, 1012 |
| 6090 | 39564789 (14807, 14808) | UNCLASSIFIED | 1022 |
| 6091 | 78394792 (14809, 14810) | UNCLASSIFIED | 1030 |
| 6092 | 82436757 (14819, 14820) | UNCLASSIFIED | 1001 |
| 6093 | 79857010 (14827, 14828) | UNCLASSIFIED | 1017 |
| 6094 | 79912418 (14833, 14834) | UNCLASSIFIED | 1003, 1024, 1039 |
| 6095 | 20610299 (14847, 14848) | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1034 |
| 6096 | 7520373 (14851, 14852) | UNCLASSIFIED | 1058 |
| 6097 | 94315759 (14861, 14862) | UNCLASSIFIED | 1044 |
| 6098 | 66042360 (14869, 14870) | UNCLASSIFIED | 1016, 1054 |
| 6099 | 28001705 (14869, 14890) | UNCLASSIFIED | 1054 |

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| 6100 | 79817946 (14897, 14898) | | | UNCLASSIFIED | 1017 |
| 6101 | 71751873 (14899, 14900) | | | UNCLASSIFIED | 1017 |
| 6102 | 46695963 (14911, 14912) | | | UNCLASSIFIED | 1055 |
| 6103 | 29679831 (14913, 14914) | | | UNCLASSIFIED | 1026 |
| 6104 | 78439125 (14921, 14922) | | | UNCLASSIFIED | 1054 |
| 6105 | 10883732 (14925, 14926) | | | UNCLASSIFIED | 1024 |
| 6106 | 79814879 (14929, 14930) | | | UNCLASSIFIED | 1017 |
| 6107 | 20182170 (14939, 14940) | | | UNCLASSIFIED | 1010 |
| 6108 | 80481798 (14941, 14942) | | | UNCLASSIFIED | 1012, 1034 |
| 6109 | 78774280 (14943, 14944) | | | UNCLASSIFIED | 1030, 1035 |
| 6110 | 79445447 (14949, 14950) | | | UNCLASSIFIED | 1024 |
| 6111 | 87464570 (14953, 14954) | | | UNCLASSIFIED | 1048 |
| 6112 | 91014513 (14973, 14974) | | | UNCLASSIFIED | 1010 |
| 6113 | 20724615 (14983, 14984) | | | UNCLASSIFIED | 1022 |
| 6114 | 20288874 (14985, 14986) | | | UNCLASSIFIED | 1034 |
| 6115 | 79470492 (14991, 14992) | | | UNCLASSIFIED | 1022 |
| 6116 | 79832064 (15013, 15014) | | | UNCLASSIFIED | 1023 |
| 6117 | 10840979 (15015, 15016) | | | UNCLASSIFIED | 1017 |

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| 6118 | 9528784 (15025, 15026) | UNCLASSIFIED | 1008 |
| 6119 | 10367865 (15047, 15048) | UNCLASSIFIED | 1034 |
| 6120 | 20290685 (15053, 15054) | UNCLASSIFIED | 1054 |
| 6121 | 65471547 (15067, 15068) | UNCLASSIFIED | 1050 |
| 6122 | 78245105 (15073, 15074) | UNCLASSIFIED | 1012 |
| 6123 | 80499691 (15075, 15076) | UNCLASSIFIED | 1030 |
| 6124 | 30169721 (15085, 15086) | UNCLASSIFIED | 1053 |
| 6125 | 27569515 (15091, 15092) | UNCLASSIFIED | 1024, 1034, 1038, 1039, 1053, 1058 |
| 6126 | 80435976 (15101, 15102) | UNCLASSIFIED | 1000 |
| 6127 | 32298653 (15113, 15114) | UNCLASSIFIED | 1038 |
| 6128 | 65474183 (15119, 15120) | UNCLASSIFIED | 1022 |
| 6129 | 20715643 (15121, 15122) | UNCLASSIFIED | 1016, 1036 |
| 6130 | 65505758 (15133, 15134) | UNCLASSIFIED | 1024 |
| 6131 | 17884741 (15135, 15136) | UNCLASSIFIED | 1010 |
| 6132 | 79445908 (15137, 15138) | UNCLASSIFIED | 1042, 1054 |
| 6133 | 65468678 (15139, 15140) | UNCLASSIFIED | 1004, 1022 |
| 6134 | 95292733 (15157, 15158) | UNCLASSIFIED | 1003, 1025, 1034, 1054 |
| 6135 | 81606240 (15169, 15170) | UNCLASSIFIED | |

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| 6136 | 52482921 (15181, 15182) | | UNCLASSIFIED | 1036 |
| 6137 | 80249237 (15185, 15186) | | UNCLASSIFIED | 1006, 1023 |
| 6138 | 85528846 (15187, 15188) | | UNCLASSIFIED | 1038 |
| 6139 | 11356609 (15193, 15194) | | UNCLASSIFIED | 1058 |
| 6140 | 8900447 (15201, 15202) | | UNCLASSIFIED | 1004 |
| 6141 | 66557173 (15207, 15208) | | UNCLASSIFIED | 1003, 1006, 1009, 1029 |
| 6142 | 17905313 (15217, 15218) | | UNCLASSIFIED | 1024 |
| 6143 | 39711115 (15265, 15266) | | UNCLASSIFIED | 1030 |
| 6144 | 80420041 (15267, 15268) | | UNCLASSIFIED | 1003, 1025 |
| 6145 | 49954326 (15279, 15280) | | UNCLASSIFIED | 1036 |
| 6146 | 27841955 (15285, 15286) | | UNCLASSIFIED | 1022 |
| 6147 | 17941363 (15303, 15304) | | UNCLASSIFIED | 1008 |
| 6148 | 29360575 (15307, 15308) | | UNCLASSIFIED | 1009 |
| 6149 | 11694135 (15323, 15324) | | UNCLASSIFIED | 1016 |
| 6150 | 20437235 (15353, 15354) | | UNCLASSIFIED | 1022 |
| 6151 | 17962664 (15375, 15376) | | UNCLASSIFIED | 1003 |
| 6152 | 37036201 (15381, 15382) | | UNCLASSIFIED | 1012 |
| 6153 | 21148407 (15393, 15394) | | UNCLASSIFIED | 1058 |

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| 6154 | 78386135 (15421, 15422) | | UNCLASSIFIED | 1058 |
| 6155 | 79233705 (15425, 15426) | | UNCLASSIFIED | 1026, 1038 |
| 6156 | 65878005 (15441, 15442) | | UNCLASSIFIED | 1037 |
| 6157 | 47662156 (15447, 15448) | | UNCLASSIFIED | 1031 |
| 6158 | 13000633 (15449, 15450) | | UNCLASSIFIED | 1008, 1016, 1024, 1054 |
| 6159 | 71214081 (15453, 15454) | | UNCLASSIFIED | 1021 |
| 6160 | 46776147 (15469, 15470) | | UNCLASSIFIED | 1024 |
| 6161 | 29522116 (15475, 15476) | | UNCLASSIFIED | 1003, 1040 |
| 6162 | 94321065 (15515, 15516) | | UNCLASSIFIED | 1022 |
| 6163 | 29465102 (15523, 15524) | | UNCLASSIFIED | 1022 |
| 6164 | 38315439 (15525, 15526) | | UNCLASSIFIED | 1022 |
| 6165 | 10332787 (15529, 15530) | | UNCLASSIFIED | 1025 |
| 6166 | 70970283 (15531, 15538) | | UNCLASSIFIED | 1037 |
| 6167 | 79253908 (15539, 15540) | | UNCLASSIFIED | 1016 |
| 6168 | 80233376 (15545, 15546) | | UNCLASSIFIED | 1006, 1022 |
| 6169 | 78971479 (15569, 15570) | | UNCLASSIFIED | 1039 |
| 6170 | 78971675 (15575, 15576) | | UNCLASSIFIED | 1017 |
| 6171 | 46777800 (15579, 15580) | | UNCLASSIFIED | 1021 |

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| 6172 | 55778366 (15685, 15586) | UNCLASSIFIED | 1021 |
| 6173 | 20617381 (15691, 15592) | UNCLASSIFIED | 1004 |
| 6174 | 79859183 (15601, 15602) | UNCLASSIFIED | 1017, 1044, 1049 |
| 6175 | 34392799 (15635, 15636) | UNCLASSIFIED | 1000 |
| 6176 | 79107926 (15645, 15646) | UNCLASSIFIED | 1023 |
| 6177 | 20288941 (15649, 15650) | UNCLASSIFIED | 1034 |
| 6178 | 78978200 (15655, 15656) | UNCLASSIFIED | 1054 |
| 6179 | 28375850 (15683, 15684) | UNCLASSIFIED | 1044 |
| 6180 | 80076624 (15691, 15692) | UNCLASSIFIED | 1003, 1008, 1029, 1034, 1038 |
| 6181 | 20272040 (15697, 15698) | UNCLASSIFIED | 1004 |
| 6182 | 30407363 (15723, 15724) | UNCLASSIFIED | 1026 |
| 6183 | 65703781 (15725, 15726) | UNCLASSIFIED | 1038 |
| 6184 | 18593385 (15727, 15728) | UNCLASSIFIED | 1008 |
| 6185 | 49555548 (15733, 15734) | UNCLASSIFIED | 1036 |
| 6186 | 15010520 (15735, 15736) | UNCLASSIFIED | 1001 |
| 6187 | 79176937 (15739, 15740) | UNCLASSIFIED | 1001 |
| 6188 | 65504551 (15741, 15742) | UNCLASSIFIED | 1016 |
| 6189 | 55504307 (15751, 15752) | UNCLASSIFIED | 1021 |

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| 6190 | 35128137 (15755, 15756) | | UNCLASSIFIED | 1012 |
| 6191 | 29361307 (15757, 15758) | | UNCLASSIFIED | 1023 |
| 6192 | 23290193 (15769, 15770) | | UNCLASSIFIED | 1003 |
| 6193 | 65706368 (15771, 15772) | | UNCLASSIFIED | 1038 |
| 6194 | 39733782 (15785, 15786) | | UNCLASSIFIED | 1026 |
| 6195 | 82097441 (15799, 15800) | | UNCLASSIFIED | 1016, 1024, 1038 |
| 6196 | 55267313 (15819, 15820) | | UNCLASSIFIED | 1054 |
| 6197 | 80050089 (15821, 15822) | | UNCLASSIFIED | 1010 |
| 6198 | 54996300 (15823, 15824) | | UNCLASSIFIED | 1029 |
| 6199 | 87453862 (15825, 15826) | | UNCLASSIFIED | 1025 |
| 6200 | 11805874 (15827, 15828) | | UNCLASSIFIED | 1022 |
| 6201 | 71755047 (15845, 15846) | | UNCLASSIFIED | 1009 |
| 6202 | 79863766 (15861, 15862) | | UNCLASSIFIED | 1017 |
| 6203 | 57568192 (15863, 15864) | | UNCLASSIFIED | 1054 |
| 6204 | 66173638 (15885, 15886) | | UNCLASSIFIED | 1016 |
| 6205 | 77664257 (15909, 15910) | | UNCLASSIFIED | 1016 |
| 6206 | 65645917 (15921, 15922) | | UNCLASSIFIED | 1041 |
| 6207 | 13506310 (15933, 15934) | | UNCLASSIFIED | 1034 |

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| 6208 | 79623652 (15947, 15948) | | UNCLASSIFIED | 1006, 1010, 1022 |
| 6209 | 79260126 (15951, 15952) | | UNCLASSIFIED | 1031 1024 |
| 6210 | 46571816 (15953, 15954) | | UNCLASSIFIED | 1029 |
| 6211 | 28775980 (15981, 15982) | | UNCLASSIFIED | 1008 |
| 6212 | 13517784 (15993, 15994) | | UNCLASSIFIED | 1024 |
| 6213 | 79628918 (16011, 16012) | | UNCLASSIFIED | 1034, 1039 |
| 6214 | 70975001 (16013, 16014) | | UNCLASSIFIED | 1023 |
| 6215 | 91234901 (16015, 16016) | | UNCLASSIFIED | 1010 |
| 6216 | 20076720 (16017, 16018) | | UNCLASSIFIED | 1006, 1054 |
| 6217 | 25261451 (16057, 16058) | | UNCLASSIFIED | 1008 |
| 6218 | 11399510 (16063, 16064) | | UNCLASSIFIED | 1006 |
| 6219 | 94238214 (16067, 16068) | | UNCLASSIFIED | 1010 |
| 6220 | 12925720 (16097, 16098) | | UNCLASSIFIED | 1024 |
| 6221 | 17941857 (16107, 16108) | | UNCLASSIFIED | 1038 |
| 6222 | 29446961 (16133, 16134) | | UNCLASSIFIED | 1026 |
| 6223 | 80054226 (16145, 16146) | | UNCLASSIFIED | 1004 |
| 6224 | 30675527 (16155, 16156) | | UNCLASSIFIED | 1030 |
| 6225 | 658861723 (16173, 16174) | | UNCLASSIFIED | 1016 |

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| 6226 | 20221778 (16191, 16192) | UNCLASSIFIED | 1034 |
| 6227 | 78251017 (16209, 16210) | UNCLASSIFIED | 1026 |
| 6228 | 65674666 (16213, 16214) | UNCLASSIFIED | 1038 |
| 6229 | 27347859 (16215, 16216) | UNCLASSIFIED | 1022 |
| 6230 | 32127312 (16217, 16218) | UNCLASSIFIED | 1029 |
| 6231 | 65903183 (16221, 16222) | UNCLASSIFIED | 1023 |
| 6232 | 78937123 (16223, 16224) | UNCLASSIFIED | 1017, 1038 |
| 6233 | 49586655 (16237, 16238) | UNCLASSIFIED | 1036 |
| 6234 | 95357326 (16251, 16252) | UNCLASSIFIED | 1054 |
| 6235 | 78062993 (16257, 16258) | UNCLASSIFIED | 1001 |
| 6236 | 80180274 (16265, 16266) | UNCLASSIFIED | 1000, 1022 |
| 6237 | 20473985 (16275, 16276) | UNCLASSIFIED | 1004, 1010 |
| 6238 | 99280757 (16281, 16282) | UNCLASSIFIED | 1001, 1010 |
| 6239 | 39727970 (16287, 16288) | UNCLASSIFIED | 1026 |
| 6240 | 65869753 (16295, 16296) | UNCLASSIFIED | 1016 |
| 6241 | 58092972 (16305, 16306) | UNCLASSIFIED | 1024 |
| 6242 | 66770570 (16317, 16318) | UNCLASSIFIED | 1023, 1049 |
| 6243 | 78687480 (16321, 16322) | UNCLASSIFIED | 1024 |

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| 6244 | 34408083 (16325, 16326) | | | UNCLASSIFIED | 1026 |
| 6245 | 66002234 (16329, 16330) | | | UNCLASSIFIED | 1010, 1054 |
| 6246 | 79912122 (16337, 16338) | | | UNCLASSIFIED | 1017 |
| 6247 | 79476974 (16351, 16352) | | | UNCLASSIFIED | 1025 |
| 6248 | 11690067 (16367, 16368) | | | UNCLASSIFIED | 1034 |
| 6249 | 19885930 (16369, 16370) | | | UNCLASSIFIED | 1001, 1004 |
| 6250 | 28368014 (16377, 16378) | | | UNCLASSIFIED | 1024 |
| 6251 | 80209869 (16381, 16382) | | | UNCLASSIFIED | 1003, 1004, 1017, 1022, 1044 |
| 6252 | 65877778 (16387, 16388) | | | UNCLASSIFIED | 1038 |
| 6253 | 34409804 (16397, 16398) | | | UNCLASSIFIED | 1026 |
| 6254 | 82491768 (16407, 16408) | | | UNCLASSIFIED | 1003, 1010, 1029 |
| 6255 | 39523348 (16409, 16410) | | | UNCLASSIFIED | 1022, 1024 |
| 6256 | 23308540 (16411, 16412) | | | UNCLASSIFIED | 1053 |
| 6257 | 49609554 (16419, 16420) | | | UNCLASSIFIED | 1036 |
| 6258 | 79927771 (16427, 16428) | | | UNCLASSIFIED | 1039 |
| 6259 | 78762359 (16431, 16432) | | | UNCLASSIFIED | 1017, 1053 |
| 6260 | 47652318 (16433, 16434) | | | UNCLASSIFIED | 1029 |
| 6261 | 10888803 (16441, 16442) | | | UNCLASSIFIED | 1031 |

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| 6262 | 70975008 (16443, 16444) | | | UNCLASSIFIED | 1023 |
| 6263 | 95416422 (16453, 16454) | | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1012, 1017, 1029, 1034, 1038, 1054 |
| 6264 | 87458994 (16469, 16470) | | | UNCLASSIFIED | 1018 |
| 6265 | 65852879 (16477, 16478) | | | UNCLASSIFIED | 1038 |
| 6266 | 91226211 (16509, 16510) | | | UNCLASSIFIED | 1013, 1020, 1053 |
| 6267 | 16390345 (16513, 16514) | | | UNCLASSIFIED | 1030 |
| 6268 | 11077618 (16519, 16520) | | | UNCLASSIFIED | 1024 |
| 6269 | 55773995 (16539, 16540) | | | UNCLASSIFIED | 1042 |
| 6270 | 11811649 (16555, 16556) | | | UNCLASSIFIED | 1025 |
| 6271 | 34891868 (16573, 16574) | | | UNCLASSIFIED | 1050 |
| 6272 | 78677624 (16575, 16576) | | | UNCLASSIFIED | 1008 |
| 6273 | 65506366 (16577, 16578) | | | UNCLASSIFIED | 1016, 1021 |
| 6274 | 20267181 (16585, 16586) | | | UNCLASSIFIED | 1034 |
| 6275 | 79976663 (16587, 16588) | | | UNCLASSIFIED | 1039 |
| 6276 | 39373467 (16593, 16594) | | | UNCLASSIFIED | 1022 |
| 6277 | 79399334 (16659, 16660) | | | UNCLASSIFIED | 1024 |
| 6278 | 30260317 (16671, 16672) | | | UNCLASSIFIED | 1008 |

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| 6279 | 46875679 (16675, 16676) | | UNCLASSIFIED | 1000 |
| 6280 | 78674442 (16679, 16680) | | UNCLASSIFIED | 1022 |
| 6281 | 27980826 (16687, 16688) | | UNCLASSIFIED | 1006 |
| 6282 | 29672933 (16689, 16690) | | UNCLASSIFIED | 1030 |
| 6283 | 12992052 (16693, 16694) | | UNCLASSIFIED | 1031 |
| 6284 | 56516463 (16703, 16704) | | UNCLASSIFIED | 1019 |
| 6285 | 11703605 (16707, 16708) | | UNCLASSIFIED | 1038 |
| 6286 | 10856407 (16709, 16710) | | UNCLASSIFIED | 1001 |
| 6287 | 94319101 (16713, 16714) | | UNCLASSIFIED | 1010 |
| 6288 | 58094076 (16727, 16728) | | UNCLASSIFIED | 1054 |
| 6289 | 79483800 (16729, 16730) | | UNCLASSIFIED | 1038 |
| 6290 | 11707576 (16811, 16812) | | UNCLASSIFIED | 1038 |
| 6291 | 78943339 (16823, 16824) | | UNCLASSIFIED | 1038 |
| 6292 | 79647741 (16825, 16826) | | UNCLASSIFIED | 1038 |
| 6293 | 78978570 (16831, 16832) | | UNCLASSIFIED | 1016 |
| 6294 | 29024905 (16835, 16836) | | UNCLASSIFIED | 1017 |
| 6295 | 80062444 (16839, 16840) | | UNCLASSIFIED | 1010 |
| 6296 | 87890476 (16851, 16852) | | UNCLASSIFIED | 1015 |

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| 6297 | 66053538 (16865, 16866) | | | UNCLASSIFIED | 1008 |
| 6298 | 20467513 (16877, 16878) | | | UNCLASSIFIED | 1010, 1024, 1034 |
| 6299 | 78256335 (16885, 16886) | | | UNCLASSIFIED | 1012, 1034 |
| 6300 | 79578444 (16889, 16890) | | | UNCLASSIFIED | 1006, 1034 |
| 6301 | 35606207 (16895, 16896) | | | UNCLASSIFIED | 1053 |
| 6302 | 65651050 (16903, 16904) | | | UNCLASSIFIED | 1054 |
| 6303 | 21426931 (16905, 16906) | | | UNCLASSIFIED | 1022 |
| 6304 | 11092942 (16907, 16908) | | | UNCLASSIFIED | 1053 |
| 6305 | 54540147 (16917, 16918) | | | UNCLASSIFIED | 1041 |
| 6306 | 80085964 (16919, 16920) | | | UNCLASSIFIED | 1054 |
| 6307 | 794211045 (16921, 16922) | | | UNCLASSIFIED | 1006 |
| 6308 | 11753810 (16925, 16926) | | | UNCLASSIFIED | 1025 |
| 6309 | 80435984 (16929, 16930) | | | UNCLASSIFIED | 1008, 1038, 1054 |
| 6310 | 79319129 (16931, 16932) | | | UNCLASSIFIED | 1006 |
| 6311 | 79642855 (16937, 16938) | | | UNCLASSIFIED | 1016, 1023, 1026, 1054 |
| 6312 | 79556912 (16953, 16954) | | | UNCLASSIFIED | 1023 |
| 6313 | 27851527 (16957, 16958) | | | UNCLASSIFIED | 1022 |
| 6314 | 55407090 (16969, 16970) | | | UNCLASSIFIED | 1021 |

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| 6315 | 33701019 (16973, 16974) | | UNCLASSIFIED | 1026 |
| 6316 | 78962410 (16977, 16978) | | UNCLASSIFIED | 1022, 1044 |
| 6317 | 78315334 (16989, 16990) | | UNCLASSIFIED | 1026 |
| 6318 | 35106114 (16993, 16994) | | UNCLASSIFIED | 1026 |
| 6319 | 29501291 (16997, 16998) | | UNCLASSIFIED | 1038 |
| 6320 | 20263112 (17001, 17002) | | UNCLASSIFIED | 1034 |
| 6321 | 87115276 (17007, 17008) | | UNCLASSIFIED | 1025 |
| 6322 | 78400129 (17009, 17010) | | UNCLASSIFIED | 1038 |
| 6323 | 79261539 (17015, 17016) | | UNCLASSIFIED | 1024 |
| 6324 | 80586929 (17029, 17030) | | UNCLASSIFIED | 1058 |
| 6325 | 20385668 (17037, 17038) | | UNCLASSIFIED | 1004 |
| 6326 | 94321867 (17039, 17040) | | UNCLASSIFIED | 1003 |
| 6327 | 27961840 (17065, 17066) | | UNCLASSIFIED | 1022 |
| 6328 | 79452020 (17077, 17078) | | UNCLASSIFIED | 1024 |
| 6329 | 24124853 (17085, 17086) | | UNCLASSIFIED | 1044 |
| 6330 | 80478691 (17095, 17096) | | UNCLASSIFIED | 1006, 1010, 1012, 1024 |
| 6331 | 30197903 (17101, 17102) | | UNCLASSIFIED | 1026 |
| 6332 | 86464845 (17117, 17118) | | UNCLASSIFIED | 1029 |

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| 6333 | 78170798 (17123, 17124) | | | UNCLASSIFIED | 1022, 1042, 1050 |
| 6334 | 87114572 (17133, 17134) | | | UNCLASSIFIED | 1025 |
| 6335 | 81854392 (17139, 17140) | | | UNCLASSIFIED | 1054 |
| 6336 | 20446483 (17147, 17148) | | | UNCLASSIFIED | 1024 |
| 6337 | 85809498 (17151, 17152) | | | UNCLASSIFIED | 1048 |
| 6338 | 86467214 (17153, 17154) | | | UNCLASSIFIED | 1029 |
| 6339 | 79921517 (17161, 17162) | | | UNCLASSIFIED | 1003 |
| 6340 | 65460344 (17183, 17184) | | | UNCLASSIFIED | 1054 |
| 6341 | 80048274 (17185, 17186) | | | UNCLASSIFIED | 1004, 1034 |
| 6342 | 10140934 (17191, 17192) | | | UNCLASSIFIED | 1025 |
| 6343 | 65474074 (17199, 17200) | | | UNCLASSIFIED | 1038 |
| 6344 | 37034577 (17205, 17206) | | | UNCLASSIFIED | 1012 |
| 6345 | 80035315 (17207, 17208) | | | UNCLASSIFIED | 1053 |
| 6346 | 86686395 (17261, 17262) | | | UNCLASSIFIED | 1019 |
| 6347 | 80159404 (17265, 17266) | | | UNCLASSIFIED | 1008, 1022 |
| 6348 | 11804069 (17279, 17280) | | | UNCLASSIFIED | 1006 |
| 6349 | 91226510 (17287, 17288) | | | UNCLASSIFIED | 1010 |
| 6350 | 78086151 (17301, 17302) | | | UNCLASSIFIED | 1033 |

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| 6351 | 94319109 (17311, 17312) | | UNCLASSIFIED | 1010, 1022, 1023, 1039, 1044 |
| 6352 | 34871792 (17319, 17320) | | UNCLASSIFIED | 1029 |
| 6353 | 27844610 (17337, 17338) | | UNCLASSIFIED | 1022 |
| 6354 | 86665887 (17351, 17352) | | UNCLASSIFIED | 1048 |
| 6355 | 79963112 (17361, 17362) | | UNCLASSIFIED | 1034 |
| 6356 | 65706749 (17367, 17368) | | UNCLASSIFIED | 1038 |
| 6357 | 27923824 (17371, 17372) | | UNCLASSIFIED | 1006 |
| 6358 | 80029712 (17383, 17384) | | UNCLASSIFIED | 1006, 1017, 1025 |
| 6359 | 20296403 (17407, 17408) | | UNCLASSIFIED | 1034 |
| 6360 | 78734259 (17419, 17420) | | UNCLASSIFIED | 1030 |
| 6361 | 79650090 (17425, 17426) | | UNCLASSIFIED | 1024, 1038 |
| 6362 | 8374659 (17429, 17430) | | UNCLASSIFIED | 1010 |
| 6363 | 20711340 (17435, 17436) | | UNCLASSIFIED | 1006 |
| 6364 | 16540826 (17443, 17444) | | UNCLASSIFIED | 1038 |
| 6365 | 79206191 (17445, 17446) | | UNCLASSIFIED | 1034 |
| 6366 | 24121926 (17449, 17450) | | UNCLASSIFIED | 1003 |
| 6367 | 65562167 (17455, 17456) | | UNCLASSIFIED | 1054 |
| 6368 | 27843884 (17457, 17458) | | UNCLASSIFIED | 1022, 1034 |

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| 6369 | 78491411 (17467, 17468) | | | UNCLASSIFIED | 1030 |
| 6370 | 20292668 (17477, 17478) | | | UNCLASSIFIED | 1034 |
| 6371 | 88329083 (17485, 17486) | | | UNCLASSIFIED | 1058 |
| 6372 | 94240512 (17491, 17492) | | | UNCLASSIFIED | 1039 |
| 6373 | 11698663 (17503, 17504) | | | UNCLASSIFIED | 1034 |
| 6374 | 79613989 (17537, 17538) | | | UNCLASSIFIED | 1034 |
| 6375 | 46805463 (17541, 17542) | | | UNCLASSIFIED | 1034 |
| 6376 | 80241251 (17555, 17556) | | | UNCLASSIFIED | 1006, 1024, 1030, 1054 |
| 6377 | 78462469 (17567, 17568) | | | UNCLASSIFIED | 1008 |
| 6378 | 10881403 (17601, 17602) | | | UNCLASSIFIED | 1016 |
| 6379 | 91228184 (17621, 17622) | | | UNCLASSIFIED | 1010 |
| 6380 | 32126348 (17625, 17626) | | | UNCLASSIFIED | 1008 |
| 6381 | 57764348 (17631, 17632) | | | UNCLASSIFIED | 1022 |
| 6382 | 46571821 (17645, 17646) | | | UNCLASSIFIED | 1029 |
| 6383 | 97983610 (17661, 17662) | | | UNCLASSIFIED | 1031 |
| 6384 | 79778328 (17667, 17668) | | | UNCLASSIFIED | 1017 |
| 6385 | 65467432 (17675, 17676) | | | UNCLASSIFIED | 1054 |
| 6386 | 65479198 (17689, 17690) | | | UNCLASSIFIED | 1054 |

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| 6387 | 25265657 (17705, 17706) | | UNCLASSIFIED | 1023 |
| 6388 | 13066093 (17707, 17708) | | UNCLASSIFIED | 1027 |
| 6389 | 80064307 (17709, 17710) | | UNCLASSIFIED | 1004, 1009, 1022, |
| 6390 | 11388460 (17717, 17718) | | UNCLASSIFIED | 1034 |
| 6391 | 94239442 (17733, 17734) | | UNCLASSIFIED | 1064 |
| 6392 | 2840359 (17745, 17746) | | UNCLASSIFIED | 1023 |
| 6393 | 78785225 (17753, 17754) | | UNCLASSIFIED | 1022 |
| 6394 | 79777158 (17769, 17770) | | UNCLASSIFIED | 1008, 1017, 1044 |
| 6395 | 23209563 (17781, 17782) | | UNCLASSIFIED | 1003 |
| 6396 | 77800216 (17785, 17786) | | UNCLASSIFIED | 1016, 1038, 1049 |
| 6397 | 79551380 (17793, 17794) | | UNCLASSIFIED | 1016, 1038 |
| 6398 | 65484487 (17795, 17796) | | UNCLASSIFIED | 1038 |
| 6399 | 3412592 (17805, 17806) | | UNCLASSIFIED | 1050 |
| 6400 | 38339218 (17815, 17816) | | UNCLASSIFIED | 1008 |
| 6401 | 39570371 (17819, 17820) | | UNCLASSIFIED | 1024 |
| 6402 | 79241990 (17835, 17836) | | UNCLASSIFIED | 1003, 1006, 1016, 1022, 1024, 1044 |
| 6403 | 79626037 (17839, 17840) | | UNCLASSIFIED | 1038 |
| 6404 | 78733552 (17833, 17834) | | UNCLASSIFIED | 1022, 1023 |

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| 6405 | 49315616 (17885, 17886) | | UNCLASSIFIED | 1036 |
| 6406 | 19880144 (17897, 17898) | | UNCLASSIFIED | 1034 |
| 6407 | 78753782 (17903, 17904) | | UNCLASSIFIED | 1003, 1029, 1053 |
| 6408 | 11668804 (17905, 17906) | | UNCLASSIFIED | 1022 |
| 6409 | 20456456 (17909, 17910) | | UNCLASSIFIED | 1010 |
| 6410 | 2413224 (17917, 17918) | | UNCLASSIFIED | 1003 |
| 6411 | 85513355 (17935, 17936) | | UNCLASSIFIED | 1049 |
| 6412 | 79488655 (17957, 17958) | | UNCLASSIFIED | 1038 |
| 6413 | 10141070 (17973, 17974) | | UNCLASSIFIED | 1016 |
| 6414 | 6568368 (17975, 17976) | | UNCLASSIFIED | 1010 |
| 6415 | 71056581 (17977, 17978) | | UNCLASSIFIED | 1024 |
| 6416 | 20472005 (17981, 17982) | | UNCLASSIFIED | 1022 |
| 6417 | 78503004 (17993, 17994) | | UNCLASSIFIED | 1026 |
| 6418 | 78767700 (18013, 18014) | | UNCLASSIFIED | 1008 |
| 6419 | 1139525 (18023, 18024) | | UNCLASSIFIED | 1006 |
| 6420 | 94999431 (18038, 18040) | | UNCLASSIFIED | 1058 |
| 6421 | 7977766 (18045, 18046) | | UNCLASSIFIED | 1001, 1008, 1017 |
| 6422 | 78377873 (18081, 18082) | | UNCLASSIFIED | 1026 |

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| 6423 | 80213899 (18063, 18064) | | | UNCLASSIFIED | 1004, 1053 |
| 6424 | 21393716 (18073, 18074) | | | UNCLASSIFIED | 1024 |
| 6425 | 20446839 (18081, 18082) | | | UNCLASSIFIED | 1024 |
| 6426 | 78466176 (18097, 18098) | | | UNCLASSIFIED | 1026 |
| 6427 | 95085670 (18105, 18106) | | | UNCLASSIFIED | 1010 |
| 6428 | 79833809 (18107, 18108) | | | UNCLASSIFIED | 1008 |
| 6429 | 66391698 (18117, 18118) | | | UNCLASSIFIED | 1003, 1004, 1016, 1040 |
| 6430 | 95354078 (18153, 18154) | | | UNCLASSIFIED | 1010, 1024 |
| 6431 | 17657563 (18157, 18158) | | | UNCLASSIFIED | 1017 |
| 6432 | 66253062 (18159, 18160) | | | UNCLASSIFIED | 1016 |
| 6433 | 30579725 (18171, 18172) | | | UNCLASSIFIED | 1009 |
| 6434 | 78984145 (18179, 18180) | | | UNCLASSIFIED | 1008 |
| 6435 | 11688384 (18183, 18184) | | | UNCLASSIFIED | 1031 |
| 6436 | 33765151 (18223, 18224) | | | UNCLASSIFIED | 1026 |
| 6437 | 65697756 (18251, 18252) | | | UNCLASSIFIED | 1037, 1038 |
| 6438 | 28358389 (18253, 18254) | | | UNCLASSIFIED | 1054 |
| 6439 | 65445206 (18255, 18256) | | | UNCLASSIFIED | 1016 |
| 6440 | 20583996 (18257, 18258) | | | UNCLASSIFIED | 1022 |

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| 6441 | 95196834 (18263, 18264) | | UNCLASSIFIED | 1054 |
| 6442 | 7947438 (18269, 18270) | | UNCLASSIFIED | 1038 |
| 6443 | 80093172 (18271, 18272) | | UNCLASSIFIED | 1023, 1024 |
| 6444 | 88095537 (18277, 18278) | | UNCLASSIFIED | 1001, 1003, 1006, 1008, 1034, 1044, 1054 |
| 6445 | 98959418 (18279, 18280) | | UNCLASSIFIED | 1003, 1010, 1044 |
| 6446 | 78799070 (18301, 18302) | | UNCLASSIFIED | 1026 |
| 6447 | 86381161 (18323, 18324) | | UNCLASSIFIED | 1053 |
| 6448 | 77968376 (18325, 18326) | | UNCLASSIFIED | 1054 |
| 6449 | 10053042 (18331, 18332) | | UNCLASSIFIED | 1044 |
| 6450 | 86684218 (18337, 18338) | | UNCLASSIFIED | 1029 |
| 6451 | 79864292 (18339, 18340) | | UNCLASSIFIED | 1001, 1038 |
| 6452 | 70620612 (18343, 18344) | | UNCLASSIFIED | 1036, 1042 |
| 6453 | 58092806 (18351, 18352) | | UNCLASSIFIED | 1038 |
| 6454 | 32428683 (18355, 18356) | | UNCLASSIFIED | 1038 |
| 6455 | 11768574 (18359, 18360) | | UNCLASSIFIED | 1038 |
| 6456 | 86477505 (18365, 18366) | | UNCLASSIFIED | 1029 |
| 6457 | 10327238 (18369, 18370) | | UNCLASSIFIED | 1038 |
| 6458 | 78674662 (18393, 18394) | | UNCLASSIFIED | 1022 |

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| 6459 | 79175833 (18397, 18398) | | UNCLASSIFIED | 1001 |
| 6460 | 46803653 (18411, 18412) | | UNCLASSIFIED | 1003 |
| 6461 | 78369480 (18413, 18414) | | UNCLASSIFIED | 1038 |
| 6462 | 37028955 (18423, 18424) | | UNCLASSIFIED | 1030 |
| 6463 | 78727258 (18425, 18426) | | UNCLASSIFIED | 1016 |
| 6464 | 38070037 (18439, 18440) | | UNCLASSIFIED | 1053 |
| 6465 | 15019257 (18441, 18442) | | UNCLASSIFIED | 1022 |
| 6466 | 39562008 (18443, 18444) | | UNCLASSIFIED | 1022 |
| 6467 | 77805342 (18479, 18480) | | UNCLASSIFIED | 1058 |
| 6468 | 80578631 (18485, 18486) | | UNCLASSIFIED | 1053 |
| 6469 | 79329498 (18487, 18488) | | UNCLASSIFIED | 1026 |
| 6470 | 30248596 (18495, 18496) | | UNCLASSIFIED | 1016 |
| 6471 | 78164304 (18499, 18500) | | UNCLASSIFIED | 1030 |
| 6472 | 65863790 (18507, 18508) | | UNCLASSIFIED | 1012 |
| 6473 | 65453754 (18531, 18532) | | UNCLASSIFIED | 1003 |
| 6474 | 79868333 (18545, 18546) | | UNCLASSIFIED | 1037 |
| 6475 | 94136642 (18547, 18548) | | | |
| 6476 | 42940779 (18583, 18584) | | | |

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| 6477 | 21412682 (18591, 18592) | | UNCLASSIFIED | 1008 |
| 6478 | 17941878 (18601, 18602) | | UNCLASSIFIED | 1003 |
| 6479 | 78374913 (18613, 18614) | | UNCLASSIFIED | 1010, 1016, 1038, 1040, 1054 |
| 6480 | 98426268 (18641, 18642) | | UNCLASSIFIED | 1026 |
| 6481 | 78461448 (18643, 18644) | | UNCLASSIFIED | 1008 |
| 6482 | 27296166 (18663, 18664) | | UNCLASSIFIED | 1016 |
| 6483 | 33744053 (18675, 18676) | | UNCLASSIFIED | 1030 |
| 6484 | 78761449 (18677, 18678) | | UNCLASSIFIED | 1022 |
| 6485 | 27842029 (18681, 18682) | | UNCLASSIFIED | 1006, 1008 |
| 6486 | 30175490 (18691, 18692) | | UNCLASSIFIED | 1037 |
| 6487 | 78085399 (18697, 18698) | | UNCLASSIFIED | 1026 |
| 6488 | 78146641 (18717, 18718) | | UNCLASSIFIED | 1022, 1054 |
| 6489 | 65686710 (18725, 18726) | | UNCLASSIFIED | 1034 |
| 6490 | 20297577 (18733, 18734) | | UNCLASSIFIED | 1012, 1024 |
| 6491 | 80501488 (18747, 18748) | | UNCLASSIFIED | 1008, 1009, 1039 |
| 6492 | 788939091 (18781, 18782) | | UNCLASSIFIED | 1015, 1025 |
| 6493 | 87890939 (18785, 18786) | | UNCLASSIFIED | 1022 |
| 6494 | 2941220 (18795, 18796) | | UNCLASSIFIED | |

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| 6495 | 29690767 (18797, 18798) | UNCLASSIFIED | 1016 |
| 6496 | 79973410 (18801, 18802) | UNCLASSIFIED | 1034, 1054 |
| 6497 | 79756471 (18811, 18812) | UNCLASSIFIED | 1004, 1022 |
| 6498 | 78029462 (18813, 18814) | UNCLASSIFIED | 1008 |
| 6499 | 54699809 (18817, 18818) | UNCLASSIFIED | 1041 |
| 6500 | 16316938 (18831, 18832) | UNCLASSIFIED | 1001 |
| 6501 | 82053350 (18833, 18834) | UNCLASSIFIED | 1006, 1012, 1016, 1034 |
| 6502 | 37004396 (18841, 18842) | UNCLASSIFIED | 1029 |
| 6503 | 79863805 (18853, 18854) | UNCLASSIFIED | 1038 |
| 6504 | 27964519 (18859, 18860) | UNCLASSIFIED | 1034 |
| 6505 | 71838508 (18903, 18904) | UNCLASSIFIED | 1030 |
| 6506 | 78268902 (18911, 18912) | UNCLASSIFIED | 1024 |
| 6507 | 65681302 (18943, 18944) | UNCLASSIFIED | 1041 |
| 6508 | 78789089 (18951, 18952) | UNCLASSIFIED | 1008 |
| 6509 | 79873330 (18957, 18958) | UNCLASSIFIED | 1003, 1017, 1034, 1054 |
| 6510 | 65894683 (18959, 18960) | UNCLASSIFIED | 1016 |
| 6511 | 17882378 (18965, 18966) | UNCLASSIFIED | 1039 |
| 6512 | 40388541 (18975, 18976) | UNCLASSIFIED | 1037 |

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| 6513 | 27843890 (18977, 18978) | | | UNCLASSIFIED | 1010, 1012, 1022, 1031, 1034, 1039 |
| 6514 | 78901850 (18985, 18986) | | | UNCLASSIFIED | 1039 |
| 6515 | 79764645 (18993, 18994) | | | UNCLASSIFIED | 1001, 1003, 1008, 1024 |
| 6516 | 78892361 (18999, 19000) | | | UNCLASSIFIED | 1017 |
| 6517 | 50887373 (19003, 19004) | | | UNCLASSIFIED | 1036 |
| 6518 | 65658644 (19005, 19006) | | | UNCLASSIFIED | 1054 |
| 6519 | 13417570 (19019, 19020) | | | UNCLASSIFIED | 1027 |
| 6520 | 79763279 (19031, 19032) | | | UNCLASSIFIED | 1008 |
| 6521 | 80385041 (19057, 19058) | | | UNCLASSIFIED | 1029 |
| 6522 | 79558281 (19059, 19060) | | | UNCLASSIFIED | 1038 |
| 6523 | 33202668 (19065, 19066) | | | UNCLASSIFIED | 1026 |
| 6524 | 20297461 (19071, 19072) | | | UNCLASSIFIED | 1034 |
| 6525 | 9849420 (19075, 19076) | | | UNCLASSIFIED | 1008 |
| 6526 | 80477772 (19079, 19080) | | | UNCLASSIFIED | 1012 |
| 6527 | 21416435 (19083, 19084) | | | UNCLASSIFIED | 1022 |
| 6528 | 87453055 (19091, 19092) | | | UNCLASSIFIED | 1025 |
| 6529 | 80067674 (19099, 19100) | | | UNCLASSIFIED | 1010 |
| 6530 | 86477696 (19109, 19110) | | | UNCLASSIFIED | 1029 |

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| 6531 | 66694504 (19117, 19118) | | UNCLASSIFIED | 1049 |
| 6532 | 30158760 (19131, 19132) | | UNCLASSIFIED | 1006, 1008, 1022, 1024 |
| 6533 | 10869231 (19133, 19134) | | UNCLASSIFIED | 1024 |
| 6534 | 13000747 (19135, 19136) | | UNCLASSIFIED | 1024 |
| 6535 | 57461768 (19137, 19138) | | UNCLASSIFIED | 1011 |
| 6536 | 78713835 (19139, 19140) | | UNCLASSIFIED | 1003 |
| 6537 | 94241436 (19141, 19142) | | UNCLASSIFIED | 1044 |
| 6538 | 19496550 (19145, 19146) | | UNCLASSIFIED | 1001 |
| 6539 | 81758497 (19151, 19152) | | UNCLASSIFIED | 1003, 1008, 1016, 1017, 1022, 1023, 1024, 1026, 1038, 1039, 1044, 1054 |
| 6540 | 16842113 (19159, 19160) | | UNCLASSIFIED | 1001, 1012, 1023, 1027 |
| 6541 | 6298182 (19167, 19168) | | UNCLASSIFIED | 1058 |
| 6542 | 38885157 (19173, 19174) | | UNCLASSIFIED | 1012 |
| 6543 | 6636021 (19181, 19182) | | UNCLASSIFIED | 1053 |
| 6544 | 3320355 (19189, 19190) | | UNCLASSIFIED | 1026 |
| 6545 | 70149940 (19193, 19194) | | UNCLASSIFIED | 1001, 1008, 1012 |
| 6546 | 78922427 (19199, 19200) | | UNCLASSIFIED | 1039 |

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| 6547 | 33188274 (19205, 19206) | | | UNCLASSIFIED | 1026 |
| 6548 | 78893753 (19209, 19210) | | | UNCLASSIFIED | 1029 |
| 6549 | 79912745 (19217, 19218) | | | UNCLASSIFIED | 1025 |
| 6550 | 301926660 (19219, 19220) | | | UNCLASSIFIED | 1008 |
| 6551 | 78475904 (19227, 19228) | | | UNCLASSIFIED | 1003 |
| 6552 | 36856730 (19241, 19242) | | | UNCLASSIFIED | 1016 |
| 6553 | 65455387 (19243, 19244) | | | UNCLASSIFIED | 1016 |
| 6554 | 79966806 (19265, 19266) | | | UNCLASSIFIED | 1054 |
| 6555 | 80082181 (19271, 19272) | | | UNCLASSIFIED | 1001, 1006, 1008, 1012, 1022, 1024, 1031 |
| 6556 | 28836988 (19273, 19274) | | | UNCLASSIFIED | 1026 |
| 6557 | 77884197 (19285, 19286) | | | UNCLASSIFIED | 1021 |
| 6558 | 11310995 (19289, 19290) | | | UNCLASSIFIED | 1034 |
| 6559 | 79551396 (19295, 19296) | | | UNCLASSIFIED | 1025 |
| 6560 | 29008809 (19297, 19298) | | | UNCLASSIFIED | 1008 |
| 6561 | 30251424 (19303, 19304) | | | UNCLASSIFIED | 1044 |
| 6562 | 10088956 (19313, 19314) | | | UNCLASSIFIED | 1017 |
| 6563 | 49955443 (19315, 19316) | | | UNCLASSIFIED | 1036 |
| 6564 | 87463300 (19321, 19322) | | | UNCLASSIFIED | 1025 |

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| 6565 | 56154672 (19355, 19356) | | | UNCLASSIFIED | 1021 |
| 6566 | 11073944 (19357, 19358) | | | UNCLASSIFIED | 1006 |
| 6567 | 29232396 (19359, 19360) | | | UNCLASSIFIED | 1008 |
| 6568 | 10879838 (19379, 19380) | | | UNCLASSIFIED | 1004 |
| 6569 | 94667725 (19385, 19386) | | | UNCLASSIFIED | 1017 |
| 6570 | 80401811 (19395, 19396) | | | UNCLASSIFIED | 1001, 1004, 1023, 1024, 1029, 1034, 1038, 1039, 1054 |
| 6571 | 79864114 (19399, 19400) | | | UNCLASSIFIED | 1012 |
| 6572 | 14223759 (19403, 19404) | | | UNCLASSIFIED | 1050 |
| 6573 | 95292755 (19405, 19406) | | | UNCLASSIFIED | 1024, 1039 |
| 6574 | 11786516 (19427, 19428) | | | UNCLASSIFIED | 1016 |
| 6575 | 52561125 (19435, 19436) | | | UNCLASSIFIED | 1017 |
| 6576 | 65703978 (19475, 19476) | | | UNCLASSIFIED | 1038 |
| 6577 | 3514465 (19487, 19488) | | | UNCLASSIFIED | 1050 |
| 6578 | 65700282 (19489, 19490) | | | UNCLASSIFIED | 1038 |
| 6579 | 25235948 (19493, 19494) | | | UNCLASSIFIED | 1003 |
| 6580 | 37034102 (19507, 19508) | | | UNCLASSIFIED | 1012 |
| 6581 | 94143303 (19511, 19512) | | | UNCLASSIFIED | 1003 |

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| 6582 | 80241965 (19537, 19538) | | UNCLASSIFIED | 1044 |
| 6583 | 9404258 (19539, 19540) | | UNCLASSIFIED | 1029 |
| 6584 | 86475898 (19555, 19556) | | UNCLASSIFIED | 1053 |
| 6585 | 65663427 (19569, 19570) | | UNCLASSIFIED | 1024 |
| 6586 | 79245319 (19573, 19574) | | UNCLASSIFIED | 1026 |
| 6587 | 27248495 (19575, 19576) | | UNCLASSIFIED | 1021 |
| 6588 | 56154814 (19577, 19578) | | UNCLASSIFIED | 1000 |
| 6589 | 32118434 (19591, 19592) | | UNCLASSIFIED | 1034 |
| 6590 | 7512127 (19599, 19600) | | UNCLASSIFIED | 1010 |
| 6591 | 95350928 (19603, 19604) | | UNCLASSIFIED | 1008 |
| 6592 | 28380672 (19619, 19620) | | UNCLASSIFIED | 1026 |
| 6593 | 78376056 (19635, 19636) | | UNCLASSIFIED | 1010 |
| 6594 | 94134724 (19639, 19640) | | UNCLASSIFIED | 1029 |
| 6595 | 78288306 (19647, 19648) | | UNCLASSIFIED | 1026 |
| 6596 | 78484226 (19657, 19658) | | UNCLASSIFIED | 1006, 1008 |
| 6597 | 78523509 (19665, 19666) | | UNCLASSIFIED | 1038 |
| 6598 | 79480843 (19669, 19670) | | UNCLASSIFIED | 1022 |
| 6599 | 21425248 (19671, 19672) | | UNCLASSIFIED | |

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| 6600 | 10144676 (19687, 19688) | | UNCLASSIFIED | 1025 |
| 6601 | 78192311 (19707, 19708) | | UNCLASSIFIED | 1009, 1038, 1054 |
| 6602 | 25133645 (19715, 19716) | | UNCLASSIFIED | 1003 |
| 6603 | 46886506 (19725, 19726) | | UNCLASSIFIED | 1037 |
| 6604 | 20456936 (19729, 19730) | | UNCLASSIFIED | 1010 |
| 6605 | 78912563 (19747, 19748) | | UNCLASSIFIED | 1039 |
| 6606 | 30539784 (19761, 19762) | | UNCLASSIFIED | 1026 |
| 6607 | 13516983 (19773, 19774) | | UNCLASSIFIED | 1024 |
| 6608 | 29686602 (19775, 19776) | | UNCLASSIFIED | 1009 |
| 6609 | 79633531 (19777, 19778) | | UNCLASSIFIED | 1038, 1039 |
| 6610 | 80239251 (19795, 19796) | | UNCLASSIFIED | 1022, 1034 |
| 6611 | 30787321 (19797, 19798) | | UNCLASSIFIED | 1001 |
| 6612 | 78742294 (19805, 19806) | | UNCLASSIFIED | 1044 |
| 6613 | 94326041 (19807, 19808) | | UNCLASSIFIED | 1044 |
| 6614 | 86462816 (19813, 19814) | | UNCLASSIFIED | 1007, 1042, 1048, 1050, 1054, 1057 |
| 6615 | 78770391 (19817, 19818) | | UNCLASSIFIED | 1017 |
| 6616 | 11420185 (19849, 19850) | | UNCLASSIFIED | 1017 |
| 6617 | 55409202 (19853, 19854) | | UNCLASSIFIED | 1021 |

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| 6618 | 65888637 (19855, 19856) | UNCLASSIFIED | 1053, 1054 |
| 6619 | 9123376 (19867, 19868) | UNCLASSIFIED | 1045 |
| 6620 | 66770598 (19871, 19872) | UNCLASSIFIED | 1010, 1049 |
| 6621 | 17944450 (19877, 19878) | UNCLASSIFIED | 1039 |
| 6622 | 78031938 (19901, 19902) | UNCLASSIFIED | 1024 |
| 6623 | 25266233 (19905, 19906) | UNCLASSIFIED | 1008 |
| 6624 | 78486558 (19909, 19910) | UNCLASSIFIED | 1026 |
| 6625 | 37011892 (19917, 19918) | UNCLASSIFIED | 1029 |
| 6626 | 77722402 (19919, 19920) | UNCLASSIFIED | 1054 |
| 6627 | 30211044 (19923, 19924) | UNCLASSIFIED | 1026 |
| 6628 | 20456147 (19925, 19926) | UNCLASSIFIED | 1010 |
| 6629 | 86684742 (19929, 19930) | UNCLASSIFIED | 1029 |
| 6630 | 78185541 (19959, 19960) | UNCLASSIFIED | 1029, 1055 |
| 6631 | 65868558 (19961, 19962) | UNCLASSIFIED | 1006, 1024 |
| 6632 | 36396119 (19963, 19964) | UNCLASSIFIED | 1001 |
| 6633 | 83743633 (19973, 19974) | UNCLASSIFIED | 1053 |
| 6634 | 28086352 (19979, 19980) | UNCLASSIFIED | 1003 |
| 6635 | 65597938 (20009, 20010) | UNCLASSIFIED | 1024, 1038 |

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| 6636 | 19880155 (20011, 20012) | | | UNCLASSIFIED | 1034 |
| 6637 | 79549290 (20023, 20024) | | | UNCLASSIFIED | 1026 |
| 6638 | 80423054 (20025, 20026) | | | UNCLASSIFIED | 1017, 1022, 1024, 1025 |
| 6639 | 10881223 (20049, 20050) | | | UNCLASSIFIED | 1025 |
| 6640 | 66254631 (20059, 20060) | | | UNCLASSIFIED | 1016 |
| 6641 | 11130341 (20063, 20064) | | | UNCLASSIFIED | 1004 |
| 6642 | 94665090 (20075, 20076) | | | UNCLASSIFIED | 1024 |
| 6643 | 29357909 (20077, 20078) | | | UNCLASSIFIED | 1022 |
| 6644 | 14999618 (20109, 20110) | | | UNCLASSIFIED | 1027 |
| 6645 | 11424294 (20111, 20112) | | | UNCLASSIFIED | 1017 |
| 6646 | 65985592 (20115, 20116) | | | UNCLASSIFIED | 1054 |
| 6647 | 85800760 (20117, 20118) | | | UNCLASSIFIED | 1025 |
| 6648 | 55180236 (20125, 20126) | | | UNCLASSIFIED | 1019 |
| 6649 | 85528662 (20127, 20128) | | | UNCLASSIFIED | 1038 |
| 6650 | 21650745 (20135, 20136) | | | UNCLASSIFIED | 1044 |
| 6651 | 78985325 (20161, 20162) | | | UNCLASSIFIED | 1017, 1022 |
| 6652 | 79193648 (20163, 20164) | | | UNCLASSIFIED | 1024 |
| 6653 | 80246711 (20169, 20170) | | | UNCLASSIFIED | 1017, 1053 |

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| 6654 | 79957653 (20175, 20176) | | UNCLASSIFIED | 1017 |
| 6655 | 80053285 (20177, 20178) | | UNCLASSIFIED | 1004, 1024, 1038 |
| 6656 | 87458132 (20179, 20180) | | UNCLASSIFIED | 1018 |
| 6657 | 788946560 (20191, 20192) | | UNCLASSIFIED | 1054 |
| 6658 | 17294320 (20193, 20194) | | UNCLASSIFIED | 1039 |
| 6659 | 95085689 (20225, 20226) | | UNCLASSIFIED | 1003 |
| 6660 | 11771339 (20239, 20240) | | UNCLASSIFIED | 1031 |
| 6661 | 16374631 (20259, 20260) | | UNCLASSIFIED | 1022, 1023 |
| 6662 | 81885897 (20279, 20280) | | UNCLASSIFIED | 1004, 1029, 1054 |
| 6663 | 79967464 (20289, 20290) | | UNCLASSIFIED | 1034 |
| 6664 | 21632244 (20313, 20314) | | UNCLASSIFIED | 1006 |
| 6665 | 79411433 (20317, 20318) | | UNCLASSIFIED | 1024 |
| 6666 | 80427583 (20319, 20320) | | UNCLASSIFIED | 1023, 1025 |
| 6667 | 80021433 (20325, 20326) | | UNCLASSIFIED | 1022 |
| 6668 | 87913201 (20329, 20330) | | UNCLASSIFIED | 1016, 1018, 1022 |
| 6669 | 80025276 (20337, 20338) | | UNCLASSIFIED | 1004 |
| 6670 | 70287218 (20353, 20354) | | UNCLASSIFIED | 1009 |
| 6671 | 95358370 (20375, 20376) | | UNCLASSIFIED | 1058 |

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| 6672 | 78685667 (20391, 20392) | UNCLASSIFIED | 1017, 1025 |
| 6673 | 30537259 (20399, 20400) | UNCLASSIFIED | 1026 |
| 6674 | 46849809 (20401, 20402) | UNCLASSIFIED | 1029 |
| 6675 | 65501280 (20411, 20412) | UNCLASSIFIED | 1016 |
| 6676 | 79759546 (20413, 20414) | UNCLASSIFIED | 1003, 1022, 1023, 1029, 1031, 1053 |
| 6677 | 66556266 (20441, 20442) | UNCLASSIFIED | 1023, 1029 |
| 6678 | 71846935 (20449, 20450) | UNCLASSIFIED | 1016, 1019, 1038 |
| 6679 | 51621152 (20453, 20454) | UNCLASSIFIED | 1036 |
| 6680 | 65897693 (20467, 20468) | UNCLASSIFIED | 1016, 1023 |
| 6681 | 10881006 (20479, 20480) | UNCLASSIFIED | 1038 |
| 6682 | 30197925 (20493, 20494) | UNCLASSIFIED | 1026 |
| 6683 | 30270530 (20501, 20502) | UNCLASSIFIED | 1008 |
| 6684 | 27976166 (20519, 20520) | UNCLASSIFIED | 1053 |
| 6685 | 5640845 (20521, 20522) | UNCLASSIFIED | 1058 |
| 6686 | 20297948 (20531, 20532) | UNCLASSIFIED | 1034 |
| 6687 | 35051908 (20533, 20534) | UNCLASSIFIED | 1022 |
| 6688 | 54701630 (20535, 20536) | UNCLASSIFIED | 1036, 1054 |
| 6689 | 98220400 (20541, 20542) | UNCLASSIFIED | 1006, 1030, 1044 |

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| 6690 | 66468057 (20543, 20544) | | UNCLASSIFIED | 1026 |
| 6691 | 23329744 (20553, 20554) | | UNCLASSIFIED | 1026 |
| 6692 | 11694506 (20557, 20558) | | UNCLASSIFIED | 1001, 1034 |
| 6693 | 87453392 (20565, 20566) | | UNCLASSIFIED | 1007, 1025 |
| 6694 | 77879679 (20581, 20582) | | UNCLASSIFIED | 1019 |
| 6695 | 56072833 (20585, 20586) | | UNCLASSIFIED | 1009 |
| 6696 | 11083544 (20599, 20600) | | UNCLASSIFIED | 1024 |
| 6697 | 33202122 (20601, 20602) | | UNCLASSIFIED | 1026 |
| 6698 | 29350591 (20619, 20620) | | UNCLASSIFIED | 1017 |
| 6699 | 21434972 (20643, 20644) | | UNCLASSIFIED | 1024 |
| 6700 | 10102678 (20647, 20648) | | UNCLASSIFIED | 1012 |
| 6701 | 79825444 (20653, 20654) | | UNCLASSIFIED | 1044 |
| 6702 | 80398431 (20669, 20670) | | UNCLASSIFIED | 1008, 1029 |
| 6703 | 20292156 (20709, 20710) | | UNCLASSIFIED | 1034 |
| 6704 | 77588735 (20743, 20744) | | UNCLASSIFIED | 1049 |
| 6705 | 20623835 (20745, 20746) | | UNCLASSIFIED | 1004 |
| 6706 | 52886465 (20759, 20760) | | UNCLASSIFIED | 1058 |
| 6707 | 78952370 (20767, 20768) | | UNCLASSIFIED | 1016 |

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| 6708 | 54527124 (20783, 20794) | | | UNCLASSIFIED | 1041 |
| 6709 | 66173662 (20789, 20790) | | | UNCLASSIFIED | 1016 |
| 6710 | 71109596 (20815, 20816) | | | UNCLASSIFIED | 1029 |
| 6711 | 20615659 (20835, 20836) | | | UNCLASSIFIED | 1004 |
| 6712 | 80248179 (20853, 20854) | | | UNCLASSIFIED | 1006 |
| 6713 | 7700013 (20857, 20858) | | | UNCLASSIFIED | 1012, 1034 |
| 6714 | 46890237 (20863, 20864) | | | UNCLASSIFIED | 1019 |
| 6715 | 79911071 (20875, 20876) | | | UNCLASSIFIED | 1038 |
| 6716 | 95292765 (20877, 20878) | | | UNCLASSIFIED | 1006, 1024 |
| 6717 | 16738239 (20879, 20880) | | | UNCLASSIFIED | 1017 |
| 6718 | 78925093 (20881, 20882) | | | UNCLASSIFIED | 1054 |
| 6719 | 10237137 (20889, 20900) | | | UNCLASSIFIED | 1039 |
| 6720 | 54986864 (20915, 20916) | | | UNCLASSIFIED | 1037 |
| 6721 | 55184965 (20923, 20924) | | | UNCLASSIFIED | 1037 |
| 6722 | 80260582 (20925, 20926) | | | UNCLASSIFIED | 1024, 1034 |
| 6723 | 37003564 (20949, 20950) | | | UNCLASSIFIED | 1029 |
| 6724 | 30650728 (20965, 20966) | | | UNCLASSIFIED | 1008 |
| 6725 | 25256741 (20967, 20968) | | | UNCLASSIFIED | 1003 |

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| 6726 | 77694079 (21005, 21006) | | | UNCLASSIFIED | 1004 |
| 6727 | 28489322 (21041, 21042) | | | UNCLASSIFIED | 1022 |
| 6728 | 65507911 (21043, 21044) | | | UNCLASSIFIED | 1038 |
| 6729 | 46874732 (21045, 21046) | | | UNCLASSIFIED | 1050 |
| 6730 | 25241134 (21051, 21052) | | | UNCLASSIFIED | 1039 |
| 6731 | 78394531 (21075, 21076) | | | UNCLASSIFIED | 1030 |
| 6732 | 65487012 (21083, 21084) | | | UNCLASSIFIED | 1023 |
| 6733 | 13084204 (21091, 21092) | | | UNCLASSIFIED | 1024 |
| 6734 | 85525183 (21093, 21094) | | | UNCLASSIFIED | 1038 |
| 6735 | 65704703 (21095, 21096) | | | UNCLASSIFIED | 1041 |
| 6736 | 90938262 (21097, 21098) | | | UNCLASSIFIED | 1020 |
| 6737 | 65861758 (21107, 21108) | | | UNCLASSIFIED | 1008, 1016, 1023, 1024, 1038, 1039, 1044, 1054 |
| 6738 | 20377410 (21109, 21110) | | | UNCLASSIFIED | 1010 |
| 6739 | 12966947 (21113, 21114) | | | UNCLASSIFIED | 1031 |
| 6740 | 85811480 (21121, 21122) | | | UNCLASSIFIED | 1019, 1054 |
| 6741 | 79242591 (21123, 21124) | | | UNCLASSIFIED | 1039 |
| 6742 | 27849426 (21133, 21134) | | | UNCLASSIFIED | 1010 |

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| 6743 | 71471627 (21135, 21136) | | | UNCLASSIFIED | 1000, 1024 |
| 6744 | 78511360 (21153, 21154) | | | UNCLASSIFIED | 1054 |
| 6745 | 20724462 (21155, 21156) | | | UNCLASSIFIED | 1006 |
| 6746 | 80257730 (21167, 21168) | | | UNCLASSIFIED | 1022 |
| 6747 | 86667153 (21175, 21176) | | | UNCLASSIFIED | 1029 |
| 6748 | 79634678 (21179, 21180) | | | UNCLASSIFIED | 1023 |
| 6749 | 10185459 (21183, 21184) | | | UNCLASSIFIED | 1003 |
| 6750 | 25322622 (21201, 21202) | | | UNCLASSIFIED | 1008 |
| 6751 | 78928316 (21203, 21204) | | | UNCLASSIFIED | 1017 |
| 6752 | 79561719 (21217, 21218) | | | UNCLASSIFIED | 1044 |
| 6753 | 66028187 (21219, 21220) | | | UNCLASSIFIED | 1003 |
| 6754 | 32116053 (21253, 21254) | | | UNCLASSIFIED | 1026 |
| 6755 | 77520607 (21261, 21262) | | | UNCLASSIFIED | 1049 |
| 6756 | 88094992 (21283, 21284) | | | UNCLASSIFIED | 1010 |
| 6757 | 79846109 (21293, 21294) | | | UNCLASSIFIED | 1034 |
| 6758 | 79600110 (21295, 21296) | | | UNCLASSIFIED | 1039 |
| 6759 | 27355032 (21303, 21304) | | | UNCLASSIFIED | 1003, 1009, 1027, 1034 |
| 6760 | 28473542 (21343, 21344) | | | UNCLASSIFIED | 1030 |

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| 6761 | 25322022 (21347, 21348) | UNCLASSIFIED | 1009 |
| 6762 | 27980692 (21349, 21350) | UNCLASSIFIED | 1006 |
| 6763 | 30158944 (21355, 21356) | UNCLASSIFIED | 1029 |
| 6764 | 79484876 (21359, 21360) | UNCLASSIFIED | 1034 |
| 6765 | 20449712 (21365, 21366) | UNCLASSIFIED | 1022 |
| 6766 | 35061023 (21371, 21372) | UNCLASSIFIED | 1054 |
| 6767 | 27976768 (21377, 21378) | UNCLASSIFIED | 1022 |
| 6768 | 19756458 (21387, 21388) | UNCLASSIFIED | 1023 |
| 6769 | 78495735 (21403, 21404) | UNCLASSIFIED | 1038 |
| 6770 | 79604896 (21409, 21410) | UNCLASSIFIED | 1039 |
| 6771 | 46801655 (21443, 21444) | UNCLASSIFIED | 1054 |
| 6772 | 65978245 (21447, 21448) | UNCLASSIFIED | 1054 |
| 6773 | 19631304 (21459, 21460) | UNCLASSIFIED | 1054 |
| 6774 | 25260354 (21465, 21466) | UNCLASSIFIED | 1026 |
| 6775 | 65703829 (21479, 21480) | UNCLASSIFIED | 1038 |
| 6776 | 23304348 (21483, 21484) | UNCLASSIFIED | 1023 |
| 6777 | 20708154 (21491, 21492) | UNCLASSIFIED | 1006 |
| 6778 | 78405682 (21493, 21494) | UNCLASSIFIED | 1016 |

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| 6779 | 7521054 (21503, 21504) | UNCLASSIFIED | 1058 |
| 6780 | 11071108 (21507, 21508) | UNCLASSIFIED | 1034 |
| 6781 | 47652347 (21525, 21526) | UNCLASSIFIED | 1029 |
| 6782 | 71820936 (21541, 21542) | UNCLASSIFIED | 1008 |
| 6783 | 87112435 (21545, 21546) | UNCLASSIFIED | 1008, 1034, 1038 |
| 6784 | 11347036 (21549, 21550) | UNCLASSIFIED | 1022 |
| 6785 | 79641410 (21557, 21558) | UNCLASSIFIED | 1038 |
| 6786 | 37419704 (21559, 21560) | UNCLASSIFIED | 1016 |
| 6787 | 10370047 (21563, 21564) | UNCLASSIFIED | 1017 |
| 6788 | 33455235 (21569, 21570) | UNCLASSIFIED | 1029 |
| 6789 | 33764191 (21571, 21572) | UNCLASSIFIED | 1026 |
| 6790 | 85800326 (21573, 21574) | UNCLASSIFIED | 1025 |
| 6791 | 20140426 (21585, 21586) | UNCLASSIFIED | 1034 |
| 6792 | 30535406 (21595, 21596) | UNCLASSIFIED | 1026 |
| 6793 | 16424745 (21597, 21598) | UNCLASSIFIED | 1038 |
| 6794 | 54701036 (21629, 21630) | UNCLASSIFIED | 1019 |
| 6795 | 20620764 (21637, 21638) | UNCLASSIFIED | 1034 |
| 6796 | 21639344 (21655, 21656) | UNCLASSIFIED | 1017 |

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| 6797 | 24128820 (21681, 21682) | | UNCLASSIFIED | 1003, 1022 |
| 6798 | 10159618 (21685, 21686) | | UNCLASSIFIED | 1001 |
| 6799 | 2328970 (21689, 21690) | | UNCLASSIFIED | 1044 |
| 6800 | 32734644 (21703, 21704) | | UNCLASSIFIED | 1001 |
| 6801 | 78369035 (21711, 21712) | | UNCLASSIFIED | 1017 |
| 6802 | 65902412 (21715, 21716) | | UNCLASSIFIED | 1023 |
| 6803 | 94233902 (21723, 21724) | | UNCLASSIFIED | 1003, 1023 |
| 6804 | 20691310 (21739, 21740) | | UNCLASSIFIED | 1010 |
| 6805 | 77801513 (21757, 21758) | | UNCLASSIFIED | 1024, 1049 |
| 6806 | 70945161 (21759, 21760) | | UNCLASSIFIED | 1029, 1057 |
| 6807 | 28461558 (21761, 21762) | | UNCLASSIFIED | 1003 |
| 6808 | 85822907 (21777, 21778) | | UNCLASSIFIED | 1048 |
| 6809 | 79834932 (21807, 21808) | | UNCLASSIFIED | 1022, 1039 |
| 6810 | 79918164 (21811, 21812) | | UNCLASSIFIED | 1039 |
| 6811 | 33267551 (21819, 21820) | | UNCLASSIFIED | 1001 |
| 6812 | 56317846 (21825, 21826) | | UNCLASSIFIED | 1008 |
| 6813 | 21659290 (21843, 21844) | | UNCLASSIFIED | 1034 |
| 6814 | 25140461 (21853, 21854) | | UNCLASSIFIED | 1026 |

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| | | | UNCLASSIFIED | 1023 |
| 6815 | 28457374 (21859, 21860) | | UNCLASSIFIED | 1003 |
| 6816 | 94321093 (21869, 21870) | | UNCLASSIFIED | 1003 |
| 6817 | 82301958 (21913, 21914) | | UNCLASSIFIED | 1001, 1053 |
| 6818 | 571118716 (21939, 21940) | | UNCLASSIFIED | 1054 |
| 6819 | 20182667 (21957, 21958) | | UNCLASSIFIED | 1010 |
| 6820 | 37060658 (21959, 21960) | | UNCLASSIFIED | 1054 |
| 6821 | 80243243 (21975, 21976) | | UNCLASSIFIED | 1016, 1022, 1026, 1030, 1038 |
| 6822 | 35137780 (21983, 21984) | | UNCLASSIFIED | 1050 |
| 6823 | 78392279 (21993, 21994) | | UNCLASSIFIED | 1038 |
| 6824 | 11694826 (21997, 21998) | | UNCLASSIFIED | 1038 |
| 6825 | 11362222 (22001, 22002) | | UNCLASSIFIED | 1024 |
| 6826 | 65470256 (22019, 22020) | | UNCLASSIFIED | 1038 |
| 6827 | 34123703 (22023, 22024) | | UNCLASSIFIED | 1050 |
| 6828 | 54992964 (22033, 22034) | | UNCLASSIFIED | 1029 |
| 6829 | 58093604 (22037, 22038) | | UNCLASSIFIED | 1054 |
| 6830 | 13524050 (22039, 22040) | | UNCLASSIFIED | 1034 |
| 6831 | 80475452 (22045, 22046) | | UNCLASSIFIED | 1012, 1034, 1053 |
| 6832 | 11011875 (22057, 22058) | | UNCLASSIFIED | 1024 |

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| 6833 | 20614211 (22061, 22062) | UNCLASSIFIED | 1022 |
| 6834 | 58090346 (22065, 22066) | UNCLASSIFIED | 1054 |
| 6835 | 66028348 (22071, 22072) | UNCLASSIFIED | 1003 |
| 6836 | 27973133 (22075, 22076) | UNCLASSIFIED | 1053 |
| 6837 | 78958511 (22077, 22078) | UNCLASSIFIED | 1008 |
| 6838 | 28849319 (22083, 22084) | UNCLASSIFIED | 1026 |
| 6839 | 28386733 (22085, 22086) | UNCLASSIFIED | 1024 |
| 6840 | 20441371 (22087, 22088) | UNCLASSIFIED | 1024 |
| 6841 | 32309249 (22097, 22098) | UNCLASSIFIED | 1029 |
| 6842 | 69931298 (22099, 22100) | UNCLASSIFIED | 1049 |
| 6843 | 805000092 (22101, 22102) | UNCLASSIFIED | 1003, 1004, 1006, 1008, 1012, 1017, 1022, 1023, 1024, 1025, 1034, 1039, 1044, 1054 |
| 6844 | 13527909 (22105, 22106) | UNCLASSIFIED | 1054 |
| 6845 | 47652190 (22109, 22110) | UNCLASSIFIED | 1029 |
| 6846 | 27372003 (22111, 22112) | UNCLASSIFIED | 1026 |
| 6847 | 78381424 (22113, 22114) | UNCLASSIFIED | 1008, 1026, 1029, 1053 |
| 6848 | 79832196 (22117, 22118) | UNCLASSIFIED | 1008, 1009, 1023 |

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|------|-----------------------------|--|--|--------------|---------------------------------------|
| 6849 | 65468206 (22133, 22134) | | | UNCLASSIFIED | 1054 |
| 6850 | 95292778 (22149, 22150) | | | UNCLASSIFIED | 1003, 1008, 1019, 1023, 1024, 1029 |
| 6851 | 66257954 (22157, 22158) | | | UNCLASSIFIED | 1038 |
| 6852 | 27365648 (22159, 22160) | | | UNCLASSIFIED | 1017 |
| 6853 | 20417133 (22161, 22162) | | | UNCLASSIFIED | 1010 |
| 6854 | 77689889 (22165, 22166) | | | UNCLASSIFIED | 1053 |
| 6855 | 29358969 (22167, 22168) | | | UNCLASSIFIED | 1022 |
| 6856 | 79640646 (22177, 22178) | | | UNCLASSIFIED | 1039 |
| 6857 | 24144678 (22179, 22180) | | | UNCLASSIFIED | 1053 |
| 6858 | 80033045 (22187, 22188) | | | UNCLASSIFIED | 1053 |
| 6859 | 778892413 (22203, 22204) | | | UNCLASSIFIED | 1036 |
| 6860 | 95290415 (22221, 22222) | | | UNCLASSIFIED | 1022 |
| 6861 | 11690923 (22233, 22234) | | | UNCLASSIFIED | 1034 |
| 6862 | 78675379 (22245, 22246) | | | UNCLASSIFIED | 1008 |
| 6863 | 46875341 (22273, 22274) | | | UNCLASSIFIED | 1037 |
| 6864 | 94989451 (22285, 22286) | | | UNCLASSIFIED | 1058 |
| 6865 | 71308289 (22313, 22314) | | | UNCLASSIFIED | 1001 |
| 6866 | 57506772 (22317, 22318) | | | UNCLASSIFIED | 1030, 1054 |

| | | | UNCLASSIFIED | 1017 |
|------|----------------------------|--|--------------|---|
| 6867 | 28386845 (22335, 22336) | | UNCLASSIFIED | 1003, 1008, 1010, 1012, 1016, 1017, 1024, 1025, 1038, 1039, 1044 |
| 6868 | 82125373 (22339, 22340) | | UNCLASSIFIED | 1027 |
| 6869 | 13089692 (22347, 22348) | | UNCLASSIFIED | 1023 |
| 6870 | 66051884 (22363, 22364) | | UNCLASSIFIED | 1022 |
| 6871 | 20287043 (22365, 22366) | | UNCLASSIFIED | 1025 |
| 6872 | 10316653 (22379, 22380) | | UNCLASSIFIED | 1054 |
| 6873 | 79254929 (22401, 22402) | | UNCLASSIFIED | 1012 |
| 6874 | 80505065 (22407, 22408) | | UNCLASSIFIED | 1008 |
| 6875 | 29026044 (22415, 22416) | | UNCLASSIFIED | 1018 |
| 6876 | 87463875 (22417, 22418) | | UNCLASSIFIED | 1022 |
| 6877 | 8227093 (22421, 22422) | | UNCLASSIFIED | 1003 |
| 6878 | 78519206 (22437, 22438) | | UNCLASSIFIED | 1030 |
| 6879 | 78762689 (22443, 22444) | | UNCLASSIFIED | 1003 |
| 6880 | 30784314 (22445, 22446) | | UNCLASSIFIED | 1034 |
| 6881 | 79439660 (22467, 22468) | | UNCLASSIFIED | 1016 |
| 6882 | 65897233 (22483, 22484) | | UNCLASSIFIED | 1017 |
| 6883 | 17707149 (22505, 22506) | | UNCLASSIFIED | |

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| | | | UNCLASSIFIED | 1004 |
| 6884 | 19636169 (22511, 22512), | | UNCLASSIFIED | 1004 |
| 6885 | 20429966 (22519, 22520), | | UNCLASSIFIED | 1004 |
| 6886 | 20623842 (22521, 22522), | | UNCLASSIFIED | 1024 |
| 6887 | 11309716 (22523, 22524), | | UNCLASSIFIED | 1010 |
| 6888 | 18514279 (22543, 22544), | | UNCLASSIFIED | 1010 |
| 6889 | 79877966 (22547, 22548), | | UNCLASSIFIED | 1025 |
| 6890 | 78749016 (22575, 22576), | | UNCLASSIFIED | 1017 |
| 6891 | 57049676 (22585, 22586), | | UNCLASSIFIED | 1009 |
| 6892 | 78762232 (22609, 22610), | | UNCLASSIFIED | 1019, 1024, 1039 |
| 6893 | 79183326 (22611, 22612), | | UNCLASSIFIED | 1001, 1003, 1024 |
| 6894 | 33188794 (22621, 22622), | | UNCLASSIFIED | 1026 |
| 6895 | 78244202 (22623, 22624), | | UNCLASSIFIED | 1017, 1026 |
| 6896 | 86685843 (22629, 22630), | | UNCLASSIFIED | 1029 |
| 6897 | 79169728 (22637, 22638), | | UNCLASSIFIED | 1024 |
| 6898 | 11304549 (22641, 22642), | | UNCLASSIFIED | 1024 |
| 6899 | 57301504 (22649, 22650), | | UNCLASSIFIED | 1004 |
| 6900 | 80428695 (22651, 22652), | | UNCLASSIFIED | 1008, 1022, 1038, 1039, 1049 |
| 6901 | 8520726 (22659, 22660), | | UNCLASSIFIED | 1024 |

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| 6902 | 29006126 (22661, 22662) | | UNCLASSIFIED | 1017 |
| 6903 | 54539432 (22673, 22674) | | UNCLASSIFIED | 1040 |
| 6904 | 80092096 (22703, 22704) | | UNCLASSIFIED | 1034 |
| 6905 | 80022300 (22729, 22730) | | UNCLASSIFIED | 1004, 1029 |
| 6906 | 35598037 (22783, 22784) | | UNCLASSIFIED | 1024 |
| 6907 | 37011599 (22795, 22796) | | UNCLASSIFIED | 1029 |
| 6908 | 78761289 (22803, 22804) | | UNCLASSIFIED | 1008, 1026 |
| 6909 | 79116899 (22851, 22852) | | UNCLASSIFIED | 1013 |
| 6910 | 78967655 (22855, 22856) | | UNCLASSIFIED | 1008, 1019, 1023, 1039 |
| 6911 | 8347474 (22859, 22860) | | UNCLASSIFIED | 1024 |
| 6912 | 65863670 (22861, 22862) | | UNCLASSIFIED | 1004 |
| 6913 | 79970189 (22875, 22876) | | UNCLASSIFIED | 1022 |
| 6914 | 13085245 (22877, 22878) | | UNCLASSIFIED | 1027 |
| 6915 | 80499553 (22881, 22882) | | UNCLASSIFIED | 1004, 1006, 1010, 1012, 1017, 1027, 1031 |
| 6916 | 86473996 (22883, 22884) | | UNCLASSIFIED | 1054 |
| 6917 | 79569041 (22887, 22888) | | UNCLASSIFIED | 1008 |
| 6918 | 79843760 (22899, 22900) | | UNCLASSIFIED | 1017 |
| 6919 | 79263014 (22911, 22912) | | UNCLASSIFIED | 1039 |

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| 6920 | 16479772 (22921, 22922) | | UNCLASSIFIED | 1003 |
| 6921 | 79840476 (22927, 22928) | | UNCLASSIFIED | 1003, 1008, 1017 |
| 6922 | 80051121 (22929, 22930) | | UNCLASSIFIED | 1004 |
| 6923 | 20289341 (22933, 22934) | | UNCLASSIFIED | 1022 |
| 6924 | 80086450 (22939, 22940) | | UNCLASSIFIED | 1010, 1019, 1041 |
| 6925 | 66368280 (22947, 22948) | | UNCLASSIFIED | 1004, 1023 |
| 6926 | 95012385 (22949, 22950) | | UNCLASSIFIED | 1010, 1025 |
| 6927 | 80188104 (22953, 22954) | | UNCLASSIFIED | 1054, 1068 |
| 6928 | 27844188 (22971, 22972) | | UNCLASSIFIED | 1024 |
| 6929 | 80234535 (17357, 17358) | Novel Protein sim. GBank gi 5031995 ref NP_005663.1 pPSCA - prostate stem cell antigen | Contains protein domain (PF00021) - u-PAR/Ly-6 domain | 1022, 1024 |
| 6930 | 78793642 (21329, 21330) | ◆ | Contains protein domain (PF00021) - u-PAR/Ly-6 domain | 1026, 1038 |
| 6931 | 50589027 (16099, 16100) | Novel Protein sim. GBank gi 2589190 (AF005081) - skin-specific protein [Homo sapiens] | Contains protein domain (PF00023) - Ank repeat | 1036 |
| 6932 | 29447258 (757, 758) | Novel Protein sim. GBank gi 5689485 dbj BA83026.1 - (AB028897) KIAA1074 protein [Homo sapiens] | Contains protein domain (PF00023) - Ank repeat | 1026 |
| 6933 | 82435190 (15703, 15704) | Novel Protein sim. GBank gi 2495617 sp Q57252 YD1J_HAEIN - HYPOTHETICAL PROTEIN HI1163 | Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron- sulfur cluster binding domains | 1001, 1004, 1006, 1017, 1022, 1024, 1039 |

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| 6934 | 49515922 (147, 148) | | Contains protein domain (PF00039) - Fibronectin type I domain | UNCLASSIFIED | 1036 |
| 6935 | 78138074 (22695, 22696) | | Contains protein domain (PF00039) - Fibronectin type I domain | UNCLASSIFIED | 1000, 1001, 1034 |
| 6936 | 78890263 (20293, 20294) | | Contains protein domain (PF00047) - Immunoglobulin domain | UNCLASSIFIED | 1024 |
| 6937 | 80584323 (7635, 7636) | Novel Protein sim. GBank gj 424025 dbj BAA74891.1 - (AB020675) KIAA0868 protein [Homo sapiens] | Contains protein domain (PF00054) - Laminin G domain | UNCLASSIFIED | 1024, 1034, 1036, 1042, 1058 |
| 6938 | 80237102 (7687, 7688) | Novel Protein sim. GBank gj 4406188 gb AAD19896 - (AF097637) group 1B pancreatic α -type secreted phospholipase A2 precursor [Mus musculus] | Contains protein domain (PF00068) - Phospholipase A2 | UNCLASSIFIED | 1006 |
| 6939 | 78743363 (6051, 6052) | Novel Protein sim. GBank gj 134611 sp P00447 SODM_YEAST - SUPEROXIDE DISMUTASE PRECURSOR (MN) | Contains protein domain (PF00081) - Iron/manganese superoxide dismutases (SODM) | UNCLASSIFIED | 1022, 1039, 1044 |
| 6940 | 79834189 (2351, 2352) | | Contains protein domain (PF00096) - Zinc finger, C2H2 type | UNCLASSIFIED | 1000, 1008, 1046 |
| 6941 | 16836028 (11589, 11590) | Novel Protein sim. GBank gj 1321818 emb CAA64725I - (X95455) RING zinc finger protein [Gallus gallus] | Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger) | UNCLASSIFIED | 1003 |
| 6942 | 80503444 (21407, 21408) | Novel Protein sim. GBank gj 137670 sp P06422 YE2 HPV08 - REGULATORY PROTEIN E2 | Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger) | UNCLASSIFIED | 1012 |
| 6943 | 25143385 (4317, 4318) | | Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger) | UNCLASSIFIED | 1008 |
| 6944 | 17087159 (20379, 20380) | Novel Protein sim. GBank gj 169927 sp P43794 GLNA_HAEIN - GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) | Contains protein domain (PF00120) - Glutamine synthetase | UNCLASSIFIED | 1023 |

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| 6945 | 87459670 (2973, 2974) | Novel Protein sim. GBank gi 121356 sp P22248 GLNA_AZ0V1 - GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) | Contains protein domain (PF00120) - Glutamine synthetase | UNCLASSIFIED | 1013, 1015 |
| 6946 | 78763247 (19409, 19410) | Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - !!! ALU SUBFAMILY SQ WARNING ENTRY !!! | Contains protein domain (PF00129) - Class I Histocompatibility antigen, domains alpha 1 and 2 | UNCLASSIFIED | 1017 |
| 6947 | 78745771 (19631, 19632) | Novel Protein sim. GBank gi 4836515 gb AAD30477.1 AF12478 - (AF124788) WS-3 protein [Mus musculus] | Contains protein domain (PF00132) - Bacterial transferase hexapeptide (four repeats) | UNCLASSIFIED | 1009 |
| 6948 | 90936873 (407, 408) | Novel Protein sim. GBank gi 2853081 emb CAAT6931.1 - (AL021768) ATP binding protein-like [Arabidopsis thaliana] | Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/rxC family | UNCLASSIFIED | 1020 |
| 6949 | 32153253 (3463, 3464) | Novel Protein sim. GBank gi 113728 sp P24735 AMPc_PSEAE - BETA-LACTAMASE PRECURSOR (CEPHALOSPORINASE) | Contains protein domain (PF00144) - Beta-lactamase | UNCLASSIFIED | 1039 |
| 6950 | 19882617 (21827, 21828) | Novel Protein sim. GBank gi 10777385 pir IS51351 - hypothetical protein YLR348c - yeast (Saccharomyces cerevisiae) | Contains protein domain (PF00153) - Mitochondrial carrier proteins | UNCLASSIFIED | 1022 |
| 6951 | 38327278 (15715, 15716) | | Contains protein domain (PF00167) - Fibroblast growth factor | UNCLASSIFIED | 1034 |
| 6952 | 37804444 (21709, 21710) | Novel Protein sim. GBank gi 249335 sp Q62261 SPCO_MOUSE - SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) | Contains protein domain (PF00169) - PH domain | UNCLASSIFIED | 1058 |
| 6953 | 86380077 (12399, 12400) | Novel Protein sim. GBank gi 2665888 (AF035948) - insulin receptor substrate-3 [Mus musculus] | Contains protein domain (PF00169) - PH domain | UNCLASSIFIED | 1053 |

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| 6954 | 80056058 (11829, 11830) | Novel Protein sim. GBank gi 731674 sp P38773 YHN3 _YEAST - HYPOTHETICAL 113.8 KD PROTEIN IN ERG7- NMD2 INTERGENIC REGION | Contains protein domain (PF00169) - PH domain | UNCLASSIFIED | 1004 |
| 6955 | 80052396 (20989, 20990) | | Contains protein domain (PF00169) - PH domain | UNCLASSIFIED | 1004 |
| 6956 | 86673218 (3991, 3992) | | Contains protein domain (PF00176) - SNF2 and others N-terminal domain | UNCLASSIFIED | 1007 |
| 6957 | 54858942 (22499, 22500) | | Contains protein domain (PF00200) - Disintegrin | UNCLASSIFIED | 1019 |
| 6958 | 27827840 (16963, 16964) | Novel Protein sim. GBank gi 940425 dbj BAA07263 - (D38069) UDP- Glucuronosyltransferase [Rattus norvegicus] | Contains protein domain (PF00201) - UDP- glucuronosyl and UDP- glucosyl transferases | UNCLASSIFIED | 1022, 1024 |
| 6959 | 36999890 (17263, 17264) | Novel Protein sim. GBank gi 1147822 (U10895) - PcaK [Pseudomonas putida] | Contains protein domain (PF00205) - Lyase | UNCLASSIFIED | 1001 |
| 6960 | 80412139 (683, 884) | Novel Protein sim. GBank gi 120602 sp P07343 FUMH_BACSU - FUMARATE HYDRATASE, CLASS-II (FUMARASE) | Contains protein domain (PF00206) - Lyase | UNCLASSIFIED | 1010, 1029 |
| 6961 | 25244080 (9255, 9256) | Novel Protein sim. GBank gi 11838 sp P2597 DCOP_BACSU - OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (OMP DECARBOXYLASE) | Contains protein domain (PF00215) - Orotidine 5'- phosphate decarboxylases | UNCLASSIFIED | 1008 |
| 6962 | 8754335 (3609, 3610) | | Contains protein domain (PF00220) - Neurohypophyseal hormones, N-terminal Domain | UNCLASSIFIED | 1004 |
| 6963 | 14997971 (9197, 9198) | | Contains protein domain (PF00220) - Neurohypophyseal hormones, N-terminal Domain | UNCLASSIFIED | 1024 |

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| 6964 | 79604083 (21899, 21900) | Novel Protein sim. GBank gil2736271 (AF028594), - Tn5501 resolvase [Pseudomonas pseudoalcaligenes] | Contains protein domain (PF00239) - Site-specific recombinases | UNCLASSIFIED | 1004 |
| 6965 | 11696111 (19549, 19550) | Novel Protein sim. GBank gil968971pir IE42463 - DNA-invertase - <i>Sigella boydii</i> | Contains protein domain (PF00239) - Site-specific recombinases | UNCLASSIFIED | 1012, 1034 |
| 6966 | 79172688 (6743, 6744) | Novel Protein sim. GBank gil4503005 ref NP_001863.1 pcPB2 - plasma carboxypeptidase B2 precursor | Contains protein domain (PF00246) - Zinc carboxypeptidase | UNCLASSIFIED | 1024 |
| 6967 | 78459354 (11657, 11658) | Novel Protein sim. GBank gil731716 spl P38836 YHT2_YEAST - HYPOTHETICAL 49.8 KD PROTEIN IN ACT3- YCK1 INTERGENIC REGION PRECURSOR | Contains protein domain (PF00246) - Zinc carboxypeptidase | UNCLASSIFIED | 1026 |
| 6968 | 78897244 (21947, 21948) | Novel Protein sim. GBank gil113580 spl P02770 ALBU_RAT - SERUM ALBUMIN PRECURSOR | Contains protein domain (PF00273) - Serum albumin family | UNCLASSIFIED | 1044 |
| 6969 | 56329560 (17671, 17672) | Novel Protein sim. GBank gil203927 (M12450) - vitamin D binding protein prepeptide [Rattus norvegicus] | Contains protein domain (PF00273) - Serum albumin family | UNCLASSIFIED | 1017 |
| 6970 | 95287765 (8673, 8674) | Novel Protein sim. GBank gil1706317 spl P31384 DCDA_MYCTU - DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE) | Contains protein domain (PF00278) - Pyridoxal- dependent decarboxylase | UNCLASSIFIED | 1008, 1012, 1034, 1036 |
| 6971 | 95005148 (1205, 1206) | Novel Protein sim. GBank gil2494176 spl Q04792 DCEH_YEAST - PUTATIVE GLUTAMATE DECARBOXYLASE (GAD) | Contains protein domain (PF00282) - Pyridoxal- dependent decarboxylase conserved domain | UNCLASSIFIED | 1003, 1034 |
| 6972 | 79173016 (1359, 1360) | | Contains protein domain (PF00288) - GHMP kinases putative ATP-binding proteins | UNCLASSIFIED | 1031 |
| 6973 | 13084179 (12333, 12334) | | Contains protein domain (PF00295) - Polygalacturonase (pectinase) | UNCLASSIFIED | 1027 |

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| 6974 10414) | 80221507 (10413) Novel Protein sim. GBank g 1348913 sp P04046 PUR1_YEAST - AMIDOPHOSPHORIBOSYLTRANSFERASE (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) | Contains protein domain (PF00310) - Glutamine amidotransferases class-II | UNCLASSIFIED | 1004, 1006, 1008, 1009, 1017, 1022, 1044 |
| 6975 94134989 (14357) 14358) | Novel Protein sim. GBank g 12494417 sp Q43139 F16Q_SACHY - FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6- BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) | Contains protein domain (PF00316) - Fructose-1,6- bisphosphatase | UNCLASSIFIED | 1003 |
| 6976 21476) | Novel Protein sim. GBank g 1351856 sp P49608 ACOC_CUCMA - ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) | Contains protein domain (PF00330) - Aconitase family (aconitate hydratase) | UNCLASSIFIED | 1007 |
| 6977 19883982 (10067, 10068) | Novel Protein sim. GBank g 1458732 dbj BA76717.1 - (AB025424) aconitase [Corynebacterium glutamicum] | Contains protein domain (PF00330) - Aconitase family (aconitate hydratase) | UNCLASSIFIED | 1001 |
| 6978 12318) | Novel Protein sim. GBank g 78222 pir A40996 - phenylalanine 4-monoxygenase (EC 1.14.16.1) - Chromobacterium violaceum | Contains protein domain (PF00351) - Bioperin- dependent aromatic amino acid hydroxylase | UNCLASSIFIED | 1039 |
| 6979 11616448 (1907, 1908) | Novel Protein sim. GBank g 1170299 sp P41809 HKR1_YEAST - HANSENIULA MRAKI KILLER TOXIN- RESISTANT PROTEIN 1 PRECURSOR | Contains protein domain (PF00357) - Integrin alpha cytoplasmic region | UNCLASSIFIED | 1024 |
| 6980 10359028 (15377, 15378) | Novel Protein sim. GBank g 2947085 U90263 - organomercural resistance regulatory protein (<i>Pseudomonas stutzeri</i>) | Contains protein domain (PF00376) - Bacterial regulatory proteins, merR family | UNCLASSIFIED | 1039 |
| 6981 78527030 (15583, 15584) | Novel Protein sim. GBank g 1234256 emb CAA74943 - (Y14603) sorbitol phosphotransferase enzyme II [Erwinia amylovora] component phosphorylation sites | Contains protein domain (PF00381) - PTS HPr component phosphorylation sites | UNCLASSIFIED | 1008, 1026 |

| | | | UNCLASSIFIED | 1038 |
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| 6982 | 10328108 (6315, 6316) | | Contains protein domain (PF00391) - PEP-utilizing enzymes | |
| 6983 | 32552724 (5573, 5574) | Novel Protein sim. GBank gli4007683lembi CAA22369] - [Al034443] putative transcriptional regulator [Streptomyces coelicolor] | Contains protein domain (PF00392) - Bacterial regulatory proteins, gntR family | 1006 |
| 6984 | 78898721 (6165, 6166) | Novel Protein sim. GBank gli2131430 pir S59790 - hypothetical protein YDR324c - yeast (Saccharomyces cerevisiae) | Contains protein domain (PF00400) - WD domain, G-beta repeat | 1039 |
| 6985 | 29246068 (9547, 9548) | Novel Protein sim. GBank gli2707295 (AF036931) - root allergen protein [Taraxacum officinale] | Contains protein domain (PF00407) - Pathogenesis-related protein Bet v 1 family | 1026 |
| 6986 | 78365892 (1845, 1846) | Novel Protein sim. GBank gli2131456 pir S61174 - hypothetical protein YDR379w - yeast (Saccharomyces cerevisiae) | Contains protein domain (PF00412) - LIM domain containing proteins | 1003 |
| 6987 | 79859913 (427, 428) | Novel Protein sim. GBank gli2983549 (AE000721) - transcriptional regulator (TetRAcrR family) [Aequifex aeolicus] | Contains protein domain (PF00440) - Bacterial regulatory proteins, tetR family | 1044 |
| 6988 | 66154240 (12229, 12230) | Novel Protein sim. GBank gli2343271 (AF014793) - pol polyprotein [walleye epidermal hyperplasia virus type 2] | Contains protein domain (PF00446) - Gonadotropin-releasing hormones | 1024 |
| 6989 | 21414443 (6979, 6980) | | Contains protein domain (PF00446) - Gonadotropin-releasing hormones | 1022 |
| 6990 | 91254670 (22049, 22050) | Novel Protein sim. GBank gli226039 pir 1408163B - CPase II B [Hordeum vulgare var. distichum] | Contains protein domain (PF00450) - Serine carboxypeptidase | 1010 |
| 6991 | 80063181 (5957, 5958) | Novel Protein sim. GBank gli2460272 (AF020809) - transcriptional activator DeoR [Salmonella typhimurium] | Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family | 1003, 1010 |

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| 6992 | 54996162 (21795, 21796) | Novel Protein sim. GBank gil3358093 sp BAAX31996 - (AB015975) Gip repressor [Pseudomonas tolaisii] | Contains protein domain (PF00465) - Bacterial regulatory proteins, deoR family | UNCLASSIFIED | 1029 |
| 6993 | 20288342 (5899, 5900) | Novel Protein sim. GBank gil1175508 sp P45388 YAEJ_PSEPU - HYPOTHETICAL 15.2 KD PROTEIN IN PCAJ 3'REGION | Contains protein domain (PF00472) - Prokaryotic-type class I peptide chain release factors | UNCLASSIFIED | 1034 |
| 6994 | 27980856 (22923, 22924) | Novel Protein sim. GBank gil1175508 sp P45388 YAEJ_PSEPU - HYPOTHETICAL 15.2 KD PROTEIN IN PCAJ 3'REGION | Contains protein domain (PF00472) - Prokaryotic-type class I peptide chain release factors | UNCLASSIFIED | 1006 |
| 6995 | 21425931 (7211, 7212) | Novel Protein sim. GBank gil1350576 sp P47349 IRF1_COXBU - PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1). | Contains protein domain (PF00472) - Prokaryotic-type class I peptide chain release factors | UNCLASSIFIED | 1022 |
| 6996 | 79582998 (17459, 17460) | Novel Protein sim. GBank gil1175188 sp P44572 Y213_HAEIN - PUTATIVE BINDING PROTEIN HI0213 PRECURSOR | Contains protein domain (PF00498) - Bacterial extracellular solute-binding proteins, family 5 | UNCLASSIFIED | 1022, 1031 |
| 6997 | 39507876 (5303, 5304) | Novel Protein sim. GBank gil2131533 sp S69559 - hypothetical protein YDR501w - yeast (Saccharomyces cerevisiae) | Contains protein domain (PF00498) - Forkhead-associated (FHA) domain | UNCLASSIFIED | 1024 |
| 6998 | 65642469 (15455, 15456) | | Contains protein domain (PF00511) - E2 (early) protein, C terminal | UNCLASSIFIED | 1016 |
| 6999 | 85519544 (13709, 13710) | Novel Protein sim. GBank gil134515 sp P17883 SK13_YEAST - SUPERKILLER 3 PROTEIN | Contains protein domain (PF00515) - TPR Domain | UNCLASSIFIED | 1001, 1003, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1025, 1026, 1027, 1034, 1038, 1039, 1044, 1049 |

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|------|--------------------------|---|--|--------------|--|
| 7000 | 25256567 (20099) | Novel Protein sim. GBank gi 38659116 (AF031609) - unknown [Oryza sativa] | Contains protein domain (PF00515) - TPR Domain | UNCLASSIFIED | 1009 |
| 7001 | 78735744 (16201, 16202) | | Contains protein domain (PF00518) - Early Protein (E6) | UNCLASSIFIED | 1009 |
| 7002 | 80074461 (17023, 17024) | Novel Protein sim. GBank gi 21314721 pir SG69891 - hypothetical protein YDR409w - yeast (Saccharomyces cerevisiae) | Contains protein domain (PF00526) - Dictyostellum (slime mold) repeats | UNCLASSIFIED | 1008, 1009, 1017, 1022, 1026, 1031 |
| 7003 | 80216295 (21511, 21512) | Novel Protein sim. GBank gi 584650 sp P38041 BOB1_YEAST - BOB1 PROTEIN (BEM1-BINDING PROTEIN) | Contains protein domain (PF00536) - SAM domain (Sterile alpha motif) | UNCLASSIFIED | 1003, 1004, 1006, 1008, 1012, 1017, 1022, 1024, 1025, 1034, 1044 |
| 7004 | 78918882 (12745, 12746) | Novel Protein sim. GBank gi 17115721 sp P55586 SUCA_ARATH - SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) | Contains protein domain (PF00549) - CoA-ligases | UNCLASSIFIED | 1039 |
| 7005 | 20287765 (14469, 14470) | Novel Protein sim. GBank gi 45121181 gb AAD21623.1 - (AF128399) succinyl-CoA synthetase alpha subunit [Pseudomonas aeruginosa] | Contains protein domain (PF00549) - CoA-ligases | UNCLASSIFIED | 1034 |
| 7006 | 17889249 (3319, 3320) | | Contains protein domain (PF00553) - Cellulose binding domain | UNCLASSIFIED | 1044 |
| 7007 | 253333573 (11123, 11124) | Novel Protein sim. GBank gi 3024880 sp O05632 Y1DE_MYCTU - HYPOTHETICAL_47_2_KD_PROTEIN_CY27_14 | Contains protein domain (PF00571) - CBS domain | UNCLASSIFIED | 1008 |
| 7008 | 80431234 (16731, 16732) | Novel Protein sim. GBank gi 3261746 emb CAB08449 - (Z95207) nusa [Mycobacterium tuberculosis] | Contains protein domain (PF00575) - S1 RNA binding domain | UNCLASSIFIED | 1004, 1006, 1010, 1012, 1022, 1023, 1024, 1031, 1034, 1038 |

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| 7009 | 79953893 (22287, 22288) | | Contains protein domain (PF00583) - Acetyltransferase (GNAT) family | UNCLASSIFIED | 1017, 1026, 1039 |
| 7010 | 80497391 (17979, 17980) | Novel Protein sim. GBank gil2909501emb[CA17386] - (AL021931) hypothetical protein Rv0380c [Mycobacterium tuberculosis] | Contains protein domain (PF00588) - SpoU rRNA Methylase family | UNCLASSIFIED | 1003, 1004, 1010, 1012, 1024, 1027, 1034 |
| 7011 | 19521786 (15213, 15214) | Novel Protein sim. GBank gil588908isp[Q05753]YACO_BACSU - HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE YACO | Contains protein domain (PF00588) - SpoU rRNA Methylase family | UNCLASSIFIED | 1034 |
| 7012 | 79859334 (2751, 2752) | Novel Protein sim. GBank gil1552728 (U70214) - ferrichrome-iron receptor precursor [Escherichia coli] | Contains protein domain (PF00593) - TonB dependent receptor C-terminal region | UNCLASSIFIED | 1017 |
| 7013 | 10870503 (5791, 5792) | Novel Protein sim. GBank gil95824 pir S09252 - ferric-coprogen receptor protein precursor - Escherichia coli | Contains protein domain (PF00593) - TonB dependent receptor C-terminal region | UNCLASSIFIED | 1031 |
| 7014 | 79831934 (2055, 2056) | Novel Protein sim. GBank gil16515isp[P22137]CLH_YEAST - CLATHRIN HEAVY CHAIN | Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS | UNCLASSIFIED | 1006, 1008 |
| 7015 | 79759680 (16601, 16602) | Novel Protein sim. GBank gil731821isp P40516 YIG4_YEAST - HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC REGION | Contains protein domain (PF00638) - RanBP1 domain. | UNCLASSIFIED | 1023 |
| 7016 | 80236362 (1293, 1294) | Novel Protein sim. GBank gil1166450emb[CAA64559] - (X95262) Tfm5 [Lycopersicon esculentum] | Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar). | UNCLASSIFIED | 1033, 1034 |
| 7017 | 9286521 (19447, 19448) | Novel Protein sim. GBank gil538258 (L01880) - elongation factor 1-gamma [Saccharomyces cerevisiae] | Contains protein domain (PF00647) - Elongation factor 1 gamma, conserved domain | UNCLASSIFIED | 1008 |

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| 7018 | 11394894 (6027, 6028) | Novel Protein sim. GBank g 1077336 pir S51467 - hypothetical protein YLR380w - yeast [Saccharomyces cerevisiae] | Contains protein domain (PF00650) - CRAL/TRIO domain. | UNCLASSIFIED | 1010 |
| 7019 | 80237349 (18083, 18084) | Novel Protein sim. GBank g 395288 emb CAA52227I - (X74130) URF [Saccharomyces cerevisiae] | Contains protein domain (PF00650) - CRAL/TRIO domain. | UNCLASSIFIED | 1010, 1017, 1022, 1034 |
| 7020 | 80496847 (12421, 12422) | Novel Protein sim. GBank g j2267235 (U69874) - delayed anaerobic 1 [Saccharomyces cerevisiae] | Contains protein domain (PF00660) - Seripauperin and TIP1 family. | UNCLASSIFIED | 1001, 1003, 1008, 1009, 1010, 1012, 1017, 1022, 1023, 1026, 1027, 1034, 1038, 1039, 1054 |
| 7021 | 80500790 (21009, 21010) | Novel Protein sim. GBank g 418400 sp P32612 PAU2_YEAST - PAU2 PROTEIN | Contains protein domain (PF00660) - Seripauperin and TIP1 family. | UNCLASSIFIED | 1004, 1006, 1010, 1012, 1022, 1023, 1024, 1025, 1029, 1031, 1034, 1038 |
| 7022 | 14401607 (13865, 13866) | Novel Protein sim. GBank g j2506427 sp Q03843 FLAA_HELPY - FLAGELLINA | Contains protein domain (PF00669) - Bacterial flagellin N-terminus | UNCLASSIFIED | 1053 |
| 7023 | 8230925 (10797, 10798) | Novel Protein sim. GBank g j731306 sp P39548 YAJ8_YEAST - HYPOTHETICAL 26.5 KD PROTEIN IN CDC15-YAT1 INTERGENIC REGION | Contains protein domain (PF00674) - DUF family of yeast membrane proteins | UNCLASSIFIED | 1022 |
| 7024 | 79423061 (1281, 1282) | Novel Protein sim. GBank g j3973254 gb AAC83237.1I - (AF072374) beta-N-acetylglucosaminidase [Pseudoalteromonas sp. S9] | Contains protein domain (PF00728) - Glycosyl hydrolase family 20 | UNCLASSIFIED | 1017 |
| 7025 | 79462065 (3727, 3728) | | Contains protein domain (PF00796) - Photosystem I reaction centre subunit VII | UNCLASSIFIED | 1034 |

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| 7026 | 78895515 (10145, 10146) | Novel Protein sim. GBank gi 3980413 (AC004561) - pumilio-like protein [Arabidopsis thaliana] | Contains protein domain (PF00806) - Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) | UNCLASSIFIED | 1023 |
| 7027 | 4922609 (15557, 15558) | | Contains protein domain (PF00807) - Apidaecin | UNCLASSIFIED | 1040 |
| 7028 | 80504167 (8393, 8394) | Novel Protein sim. GBank gi 5491041 sp P35880 TRA1_LACHE - TRANSPOSEASE FOR INSERTION SEQUENCE ELEMENT IS1201 | Contains protein domain (PF00872) - Transposase, Mutator family | UNCLASSIFIED | 1072 |
| 7029 | 66238458 (755, 756) | Novel Protein sim. GBank gi 5491051 sp P35882 TRA1_MYCTU - TRANSPOSEASE FOR INSERTION SEQUENCE ELEMENT IS1081 | Contains protein domain (PF00872) - Transposase, Mutator family | UNCLASSIFIED | 1010 |
| 7030 | 6427565 (18101, 18102) | Novel Protein sim. GBank gi 5491151 sp P35879 TRA_CORDI - PROBABLE TRANSPOSEASE FOR INSERTION SEQUENCE ELEMENT | Contains protein domain (PF00872) - Transposase, Mutator family | UNCLASSIFIED | 1058 |
| 7031 | 78937340 (22893, 22894) | Novel Protein sim. GBank gi 2983282 (AE000702) - cation efflux system (AcrB/AcrD/AcrF family) [Aequifex aeolicus] | Contains protein domain (PF00873) - AcrB/AcrD/AcrF family | UNCLASSIFIED | 1039 |
| 7032 | 65707976 (10013, 10014) | | Contains protein domain (PF00873) - AcrB/AcrD/AcrF family | UNCLASSIFIED | 1023 |
| 7033 | 87453741 (21577, 21578) | Novel Protein sim. GBank gi 3687389 emb CAA76074 - ('16124) putative cullin protein [Lycopersicon esculentum] | Contains protein domain (PF00888) - Cullin family | UNCLASSIFIED | 1025 |
| 7034 | 27804713 (11325, 11326) | Novel Protein sim. GBank gi 4503151 ref NP_03583.1 pCUL1 - cullin 1 | Contains protein domain (PF00888) - Cullin family | UNCLASSIFIED | 1024, 1034, 1039 |
| 7035 | 80233839 (1951, 1952) | Novel Protein sim. GBank gi 5139634 emb CAAB45563.1 - (AL079353) putative penicillin-binding protein [Streptomyces coelicolor] | Contains protein domain (PF00912) - Transglycosylase | UNCLASSIFIED | 1006, 1008, 1010, 1017, 1026, 1038, 1039 |

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| 7036 | 79906077 (20757, 20758) | Novel Protein sim. GBank gii2995295 emb CAA18324] - (AL022268) hypothetical protein SC4H2.08 [Streptomyces coelicolor] | Contains protein domain (PF00919) - Uncharacterized protein family UPF0004 | UNCLASSIFIED | 1012, 1023 |
| 7037 | 95292844 (5631, 5632) | Novel Protein sim. GBank gii3294240 emb CAA19853] - (AL031031) hypothetical protein SC7C7.07 [Streptomyces coelicolor] | Contains protein domain (PF00919) - Uncharacterized protein family UPF0004 | UNCLASSIFIED | 1006, 1010, 1024 |
| 7038 | 78942693 (16873, 16874) | | Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a | UNCLASSIFIED | 1038 |
| 7039 | 37803971 (5097, 5098) | Novel Protein sim. GBank gii631857 pir A41558 - N-syndecan - rat (fragment) | Contains protein domain (PF01034) - Syndecan domain | UNCLASSIFIED | 1058 |
| 7040 | 78678192 (17715, 17716) | Novel Protein sim. GBank gii1074872 pir C641173 - hypothetical protein HI1627 - Haemophilus influenzae (strain Rd KW20) | Contains protein domain (PF01042) - Domain of unknown function | UNCLASSIFIED | 1008, 1017 |
| 7041 | 19879670 (13791, 13792) | Novel Protein sim. GBank gii3820514 (AF061751) -LysR-type transcriptional regulator PhnS [Burkholderia sp. RP007] | Contains protein domain (PF01046) - NodD transcription activator carboxyl terminal region | UNCLASSIFIED | 1034 |
| 7042 | 47656797 (11407, 11408) | Novel Protein sim. GBank gii586346 spl P38138 YB79_YEAST - PUTATIVE FAMILY 31 GLUCOSIDASE IN PCS60-ABD1 INTERGENIC REGION | Contains protein domain (PF01055) - Glycosyl hydrolases family 31 | UNCLASSIFIED | 1029 |
| 7043 | 79162929 (18741, 18742) | Novel Protein sim. GBank gii54420387 emb CAB46879_1] - (A)J243459 proteophosphoglycan [Leishmania major] | Contains protein domain (PF01106) - NirU-like domain | UNCLASSIFIED | 1004, 1026, 1044 |
| 7044 | 17900428 (17557, 17558) | Novel Protein sim. GBank gii1169716 spl P44788 SUN_HAEIN - SUN PROTEIN (FMU PROTEIN) | Contains protein domain (PF01189) - NOL1/NOP2/sun family | UNCLASSIFIED | 1031, 1044 |

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| 7045 | 79600399 (2459, 2460) | Novel Protein sim. GBank gil128399ispIP14743(NMT_YEAST - GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE (PEPTIDE N-MYRISTOYLTRANSFERASE) (MYRISTOYL-COA:PROTEIN N-MYRISTOYLTRANSFERASE) (NMT) | Contains protein domain (PF01233) - Myristoyl-CoA:protein N-myristoyltransferase | | |
| 7046 | 87453362 (16123, 16124) | Novel Protein sim. GBank gil462195ispIP33278SUJ1_ORYSA - PROTEIN TRANSLATION FACTOR SUJ1 HOMOLOG (GOS2 PROTEIN) | Contains protein domain (PF01253) - Translation initiation factor SUJ1 | UNCLASSIFIED | 1022, 1025 |
| 7047 | 78985624 (6401, 6402) | Novel Protein sim. GBank gil230281lpdb1R69] - 434 Repressor (Amino-Terminal Domain) (R1-69) | Contains protein domain (PF01381) - Helix-turn-helix | UNCLASSIFIED | 1016, 1022 |
| 7048 | 13883824 (13601, 13602) | Novel Protein sim. GBank gil4154729 (AE001459) - putative [Helicobacter pylori J99] | Contains protein domain (PF01402) - Helix-turn-helix protein, copG family | UNCLASSIFIED | 1053 |
| 7049 | 80245946 (7697, 7698) | Novel Protein sim. GBank gil172947 / J03965] - Phe-tRNA synthetase [Saccharomyces cerevisiae] | Contains protein domain (PF01409) - tRNA synthetases class II (F) | UNCLASSIFIED | 1003, 1006, 1008, 1022, 1034, 1044 |
| 7050 | 79167929 (21197, 21198) | Novel Protein sim. GBank gil3880625IembICAB07858] - (Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge... | Contains protein domain (PF01412) - Putative GTPase activating protein for Arf | UNCLASSIFIED | 1031, 1050 |
| 7051 | 78471143 (7969, 7970) | Novel Protein sim. GBank gil4582434gb AAD24820.1 AC00719 - (AC007196) unknown protein [Arabidopsis thaliana] | Contains protein domain (PF01423) - Sm protein | UNCLASSIFIED | 1053 |
| 7052 | 46693429 (14041, 14042) | Novel Protein sim. GBank gil320483pir C60634 - probable transposase IS257/3 - Staphylococcus aureus plasmid pSH6 | Contains protein domain (PF01438) - Transposase | UNCLASSIFIED | 1034 |

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| 7053 | 65466599 (1925, 1926) | Novel Protein sim. GBank g 4753138 gb AAD28804.1 - (U52844) KdIB [<i>Serratia marcescens</i>] | Contains protein domain (PF01467) - Cytidyltransferase | UNCLASSIFIED | 1010 |
| 7054 | 80045310 (5257, 5258) | Novel Protein sim. GBank g 568984 emb CAE52047.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)] | Contains protein domain (PF01479) - S4 domain | UNCLASSIFIED | 1006, 1024, 1034, 1038, 1054 |
| 7055 | 54820637 (18225, 18226) | Novel Protein sim. GBank g 481462 pir S38653 - transposase - <i>Klebsiella pneumoniae</i> | Contains protein domain (PF01526) - Transposase | UNCLASSIFIED | 1029 |
| 7056 | 79258045 (1259, 1260) | Novel Protein sim. GBank g 2 32817 pir S61981 - probable membrane protein YOL003c - yeast (<i>Saccharomyces cerevisiae</i>) | Contains protein domain (PF01529) - DHHC zinc finger domain | UNCLASSIFIED | 1003, 1008, 1009 |
| 7057 | 13521641 (16399, 16400) | | Contains protein domain (PF01581) - FMRFamide related peptide family | UNCLASSIFIED | 1024 |
| 7058 | 20293179 (17, 18) | Novel Protein sim. GBank g 3122208 isp Q49776 HS1_MYCLE - ATP PHOSPHORIBOSYLTRANSFERASE | Contains protein domain (PF01634) - ATP phosphoribosyltransferase | UNCLASSIFIED | 1034 |
| 7059 | 79815141 (10003, 10004) | Novel Protein sim. GBank g 2076670 emb CAE08387 - (Z95150) hypothetical protein Rv3095 [Mycobacterium tuberculosis] | Contains protein domain (PF01638) - Protein of unknown function | UNCLASSIFIED | 1044 |
| 7060 | 13085662 (6503, 6504) | Novel Protein sim. GBank g 140807 isp P24536 Y121_BURCE - INSERTION ELEMENT IS402_HYPOTHETICAL 24 KD PROTEIN | Contains protein domain (PF01675) - Transposase | UNCLASSIFIED | 1027 |
| 7061 | 80306881 (22435, 22436) | Novel Protein sim. GBank g 1175962 isp P43545 SNZ3_YEAST - SNZ3 PROTEIN | Contains protein domain (PF01680) - Uncharacterized protein family SNZ | UNCLASSIFIED | 1001, 1003, 1006, 1008, 1009, 1012, 1017, 1022, 1023, 1024, 1026, 1029, 1031, 1034, 1044, 1053 |

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| 7062 | 13901544 (22701, 22702) | Novel Protein sim. GBank gil2501577 sp Q03148 SNZ1_YEAST - SNZ1 PROTEIN (P35) | Contains protein domain (PF01680) - Uncharacterized protein family SNZ | UNCLASSIFIED | 1053 |
| 7063 | 95293073 (1365, 1366) | Novel Protein sim. GBank gil14088 sp P27847 YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQL PLDB INTERGENIC REGION (F138) | Contains protein domain (PF01810) - LysE type translocator | UNCLASSIFIED | 1024 |
| 7064 | 78695814 (237, 238) | Novel Protein sim. GBank gil1001388 dbj BAA10878 - (D64006) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1003 |
| 7065 | 9842251 (4811, 4812) | Novel Protein sim. GBank gil1001430 dbj BAA10054 - (D63999) ORF1 [Synechocystis sp.] | | UNCLASSIFIED | 1039 |
| 7066 | 80081532 (12373, 12374) | Novel Protein sim. GBank gil1001462 dbj BAA10088 - (D63999) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1034 |
| 7067 | 16398835 (15325, 15326) | Novel Protein sim. GBank gil1001499 dbj BAA10124 - (D64000) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1003 |
| 7068 | 80051064 (2749, 2750) | Novel Protein sim. GBank gil1001663 dbj BAA10397 - (D64002) rare lipoprotein A [Synechocystis sp.] | | UNCLASSIFIED | 1004, 1010 |
| 7069 | 57301027 (2691, 2692) | Novel Protein sim. GBank gil1001939 (U13152), guanine nucleotide-binding protein beta 5 [Mesocricetus auratus] | | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1024, 1034, 1044 |
| 7070 | 79187134 (7223, 7224) | Novel Protein sim. GBank gil1006592 dbj BAA10745 - (D64005) magnesium and cobalt transport protein [Synechocystis sp.] | | UNCLASSIFIED | 1024 |
| 7071 | 80237636 (12631, 12632) | Novel Protein sim. GBank gil101245 sp S15038 - cell division control protein CDC15 - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1001, 1004, 1006, 1009, 1025, 1026, 1034 |

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| 7072 | 78376629 (7516) | Novel Protein sim. GBank gil102058 pir C41710 - promastigote surface antigen-2 (clone 2.5) - Leishmania major (fragment) | | UNCLASSIFIED | 1003 |
| 7073 | 80503459 (22669, 22670) | Novel Protein sim. GBank gil102427 pir D41132 - collagen-related protein 4 - <i>Hydra magnipapillata</i> (fragment) | | UNCLASSIFIED | 1003, 1006, 1008, 1009, 1010, 1012, 1016, 1022, 1023, 1034, 1044, 1049 |
| 7074 | 32309196 (13443, 13444) | Novel Protein sim. GBank gil106040 pir A38530 - fragile X mental retardation syndrome protein FMR1 - human (fragment) | | UNCLASSIFIED | 1029 |
| 7075 | 30537137 (3567, 3568) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1026 |
| 7076 | 54700862 (4167, 4168) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1036 |
| 7077 | 30530736 (8071, 8072) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1026 |
| 7078 | 55894344 (10621, 10622) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1038 |
| 7079 | 86665724 (21537, 21538) | Novel Protein sim. GBank gil106322 pir B34087 - hypothetical protein (L1H 3' region) - human | | UNCLASSIFIED | 1029 |
| 7080 | 23286017 (14673, 14674) | Novel Protein sim. GBank gil106323 pir A34087 - hypothetical protein (L1H 5' region) - human | | UNCLASSIFIED | 1003 |
| 7081 | 77879807 (12881, 12882) | Novel Protein sim. GBank gil106903 pir B28096 - line-1 protein ORF2 - human | | UNCLASSIFIED | 1019 |

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| 7082 | 94137421 (16359, 16360) | Novel Protein sim. GBank gil106903 pir B28096 - line-1 protein ORF2 - human | | UNCLASSIFIED | 1016, 1044 |
| 7083 | 33205928 (22903, 22904) | Novel Protein sim. GBank gil1072396 pir CAA63735.1 - (X93358) phaB [Sinorhizobium meliloti] | | UNCLASSIFIED | 1026 |
| 7084 | 20733832 (18513, 18514) | Novel Protein sim. GBank gil1072397 pir CAA63736.1 - (X93358) phaC [Sinorhizobium meliloti] | | UNCLASSIFIED | 1006 |
| 7085 | 79833309 (17331, 17332) | Novel Protein sim. GBank gil1074127 pir D64108 - gluconate permease (gntP) homolog - Haemophilus influenzae (strain Rd KW20) | | UNCLASSIFIED | 1023 |
| 7086 | 13083321 (1795, 1796) | Novel Protein sim. GBank gil1074506 pir C64158 - hypothetical protein HI0755 - Haemophilus influenzae (strain Rd KW20) | | UNCLASSIFIED | 1031 |
| 7087 | 54856328 (11431, 11432) | Novel Protein sim. GBank gil1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii | | UNCLASSIFIED | 1019 |
| 7088 | 29347055 (4003, 4004) | Novel Protein sim. GBank gil1076666 pir S51839 - D13F(MYBST1) protein - potato | | UNCLASSIFIED | 1022 |
| 7089 | 30631920 (6269, 6270) | Novel Protein sim. GBank gil1076660 pir S51839 - D13F(MYBST1) protein - potato | | UNCLASSIFIED | 1022 |
| 7090 | 65654694 (12199, 12200) | Novel Protein sim. GBank gil1076802 pir S49915 - extensin-like protein - maize | | UNCLASSIFIED | 1054 |
| 7091 | 11306338 (19461, 19462) | Novel Protein sim. GBank gil1076996 pir S49755 - adenine phosphoribosyltransferase (EC 2.4.2.7) 1 - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1024 |
| 7092 | 78759044 (6201, 8202) | Novel Protein sim. GBank gil1077123 pir S50383 - gamma-glutamyltransferase homolog YLR239w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1017, 1044 |

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| 7093 10670) | 79915055 (10669, Novel Protein sim. GBank gil1077123 pir S50383 gamma-glutamyltransferase homolog YLR299w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1017 |
| 7094 14030) | 25335671 (14029, Novel Protein sim. GBank gil1077162 pir S52504 - probable membrane protein YDL015c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1039 |
| 7095 12972) | 78787902 (12971, Novel Protein sim. GBank gil1077164 pir S52500 - SWH1 protein homolog YDL019c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1026 |
| 7096 17902) | 94996339 (17901, Novel Protein sim. GBank gil1077164 pir S52500 - SWH1 protein homolog YDL019c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1034 |
| 7097 2846) | 79242609 (2845, Novel Protein sim. GBank gil1077187 pir S49777 - probable membrane protein YDR180w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1017 |
| 7098 22758) | 10167049 (22757, Novel Protein sim. GBank gil1077257 pir S52522 - hypothetical protein YPL009c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1034 |
| 7099 6574) | 78778585 (6573, Novel Protein sim. GBank gil1077258 pir S52524 - probable membrane protein YPL007c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1009 |
| 7100 18498) | 30274057 (18497, Novel Protein sim. GBank gil1077258 pir S52524 - probable membrane protein YPL007c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1026 |
| 7101 1596) | 29354457 (1595, Novel Protein sim. GBank gil1077307 pir S51892 - probable membrane protein YOL105c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003 |

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| 7102 | 79316556 (11869 11870) | Novel Protein sim. GBank gil1077324 pir S50965 - probable membrane protein YLL055w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1004 |
| 7103 | 79398033 (3937, 3938) | Novel Protein sim. GBank gil1077335 pir S51468 - probable membrane protein YLR381w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006 |
| 7104 | 80218264 (8285, 8286) | Novel Protein sim. GBank gil1077350 pir S50381 - probable membrane protein YLR297w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1001, 1009, 1022, 1023, 1039 |
| 7105 | 80503416 (17911, 17912) | Novel Protein sim. GBank gil1077361 pir S51391 - probable membrane protein YLR373c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1004, 1008, 1009, 1012, 1017, 1023, 1024, 1030, 1038, 1044 |
| 7106 | 38869284 (20811 20812) | Novel Protein sim. GBank gil1077361 pir S51391 - probable membrane protein YLR373c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1026 |
| 7107 | 82060755 (10721, 10722) | Novel Protein sim. GBank gil1077393 pir S51403 - probable membrane protein YLR266c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1008, 1012, 1016, 1022, 1034 |
| 7108 | 10205513 (6135, 6136) | Novel Protein sim. GBank gil1077401 pir S51413 - probable membrane protein YLR277c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006 |
| 7109 | 65694968 (22593, 22594) | Novel Protein sim. GBank gil1077404 pir S51422 - probable membrane protein YLR177w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1038 |
| 7110 | 78938649 (12835, 12836) | Novel Protein sim. GBank gil1077407 pir S51435 - hypothetical protein YLR190w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1022, 1044 |

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| 7111 | 82342298 (3041, 3042) | Novel Protein sim. GBank g 1077412 pir S51432 - hypothetical protein YLR187w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1001 |
| 7112 | 65892183 (14115, 14116) | Novel Protein sim. GBank g 1077416 pir S51464 - probable membrane protein YLR356w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006, 1016 |
| 7113 | 65482988 (3263, 3264) | Novel Protein sim. GBank g 1077417 pir S51460 - hypothetical protein YLR352w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1023 |
| 7114 | 39375938 (19281, 19282) | Novel Protein sim. GBank g 1077551 pir S54034 - probable membrane protein YDR049w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1010 |
| 7115 | 78792449 (17545, 17546) | Novel Protein sim. GBank g 1077705 pir S50633 - hypothetical protein YER130c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1009 |
| 7116 | 30265873 (633, 634) | Novel Protein sim. GBank g 1077900 pir S57113 - BUD4 protein - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1026 |
| 7117 | 78758427 (3415, 3416) | Novel Protein sim. GBank g 1078071 pir S53398 - hypothetical protein YLR320w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1009, 1026, 1044 |
| 7118 | 79861629 (21087, 21088) | Novel Protein sim. GBank g 1078081 pir S53392 - probable membrane protein YLR313c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1022, 1038 |
| 7119 | 78890389 (12681, 12682) | Novel Protein sim. GBank g 1078147 pir S54389 - NCA2 protein - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1039 |
| 7120 | 28488943 (9767, 9768) | Novel Protein sim. GBank g 1078508 pir S54840 - KCS1 protein - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1023 |
| 7121 | 56147697 (21979, 21980) | Novel Protein sim. GBank g 1082459 pir A55641 - homeotic protein GAX - human | UNCLASSIFIED | 1023 |

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| 7122 | 27843871 (15223) 15224) | Novel Protein sim. GBank gil1083428 pir S54876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse | | UNCLASSIFIED | 1004, 1009, 1010, 1022, 1034 |
| 7123 | 78378457 (11711, 11712) | Novel Protein sim. GBank gil1084084 pir S55811 - hrpA protein - Escherichia coli | | UNCLASSIFIED | 1026 |
| 7124 | 19637731 (1019, 1020) | Novel Protein sim. GBank gil1084564 pir S52597 - probable membrane protein YHR070c-a - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006 |
| 7125 | 27929546 (5069, 5070) | Novel Protein sim. GBank gil1084595 pir S53561 - probable membrane protein YAL056c-a - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006 |
| 7126 | 80258617 (13919, 13920) | Novel Protein sim. GBank gil1084783 pir S54079 - BRR1 protein - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1010, 1022, 1034, 1038 |
| 7127 | 79256123 (5079, 5080) | Novel Protein sim. GBank gil1110587 bbs 170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.] | | UNCLASSIFIED | 1003, 1029 |
| 7128 | 80428421 (5623, 5624) | Novel Protein sim. GBank gil1110587 bbs 170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.] | | UNCLASSIFIED | 1003, 1010, 1024, 1025, 1053 |
| 7129 | 80061887 (8855, 8856) | Novel Protein sim. GBank gil1110587 bbs 170532 - (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.] | | UNCLASSIFIED | 1034 |

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| 7130 | 2902667 (15549, 15550) | Novel Protein sim. GBank g 1110587 bbs 170532 (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.] | UNCLASSIFIED | 1017 |
| 7131 | 78251974 (16655, 16656) | Novel Protein sim. GBank g 1110587 bbs 170532 (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.] | UNCLASSIFIED | 1026 |
| 7132 | 78461462 (21339, 21340) | Novel Protein sim. GBank g 1110587 bbs 170532 (S79410) nuclear localization signals (NLS)-binding protein=spot-1 [mice, Balb/c, testes, Peptide, 140 aa] [Mus sp.] | UNCLASSIFIED | 1003 |
| 7133 | 98220393 (15237, 15238) | Novel Protein sim. GBank g 111134 pir S22934 - testis-specific protein (clone 46) - mouse (fragment) | UNCLASSIFIED | 1026, 1031 |
| 7134 | 20608237 (3281, 3282) | Novel Protein sim. GBank g 113450 sp P07248 ADR1_YEAST - REGULATORY PROTEIN ADR1 | UNCLASSIFIED | 1004, 1022 |
| 7135 | 66489949 (591, 592) | Novel Protein sim. GBank g 113620 sp P11604 ALF_ECOLI - FRUCTOSE-BISPHOSPHATE ALDOLASE CLASS II | UNCLASSIFIED | 1029 |
| 7136 | 21436050 (17323, 17324) | Novel Protein sim. GBank g 113670 sp P23963 ALU_HUMAN - !!! ALU CLASS E WARNING ENTRY !!! | UNCLASSIFIED | 1022 |
| 7137 | 8754246 (12355, 12356) | Novel Protein sim. GBank g 113751 sp P15034 AMPP_ECOLI - XAA-PRO AMINOPEPTIDASE (X-PRO AMINOPEPTIDASE) (AMINOPEPTIDASE P II) (APP_PII) (AMINOACYLPROLINE AMINOPEPTIDASE) | UNCLASSIFIED | 1004 |
| 7138 | 79633247 (19999, 20000) | Novel Protein sim. GBank g 114113 sp P13981 ARCA_PSEAE - ARGININE DEIMINASE | UNCLASSIFIED | 1022, 1038 |

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| 7139 | 30243994 (3187, 3188) | Novel Protein sim. GBank gi 114947 sp P16279 BGAM_HUMAN - HUMAN - BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR | | UNCLASSIFIED | 1026 |
| 7140 | 80188931 (16557, 16558) | Novel Protein sim. GBank gi 115910 sp P16522 CC23_YEAST - CELL DIVISION CONTROL PROTEIN 23 | | UNCLASSIFIED | 1058 |
| 7141 | 27962453 (20491, 20492) | Novel Protein sim. GBank gi 115914 sp P04821 CC25_YEAST - CELL DIVISION CONTROL PROTEIN 25 | | UNCLASSIFIED | 1034 |
| 7142 | 25321510 (22815, 22816) | Novel Protein sim. GBank gi 115936 sp P06103 IF3X_YEAST - EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3 P90) (CELL CYCLE REGULATION AND TRANSLATION INITIATION PROTEIN) | | UNCLASSIFIED | 1022 |
| 7143 | 29345595 (4595, 4596) | Novel Protein sim. GBank gi 116515 sp P22137 CLH_YEAST - CLATHRIN HEAVY CHAIN | | UNCLASSIFIED | 1006, 1012, 1022, 1031, 1054 |
| 7144 | 80060929 (3471, 3472) | Novel Protein sim. GBank gi 1168262 sp P44425 AAT_HAEIN - ASPARTATE AMINOTRANSFERASE (TRANSAMINASE A) (ASPAT) | | UNCLASSIFIED | 1008, 1017, 1024, 1044 |
| 7145 | 10209161 (12847, 12848) | Novel Protein sim. GBank gi 116816 sp P30665 CC54_YEAST - CELL DIVISION CONTROL PROTEIN 54 | | UNCLASSIFIED | 1025 |
| 7146 | 80224008 (6259, 6260) | Novel Protein sim. GBank gi 116915 sp P08678 CYAA_YEAST - ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) | | UNCLASSIFIED | 1006, 1023, 1024, 1027 |
| 7147 | 17963110 (16817, 16818) | Novel Protein sim. GBank gi 1169152 sp P40127 CYAA_YERPE - ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) | | UNCLASSIFIED | 1038 |

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| 7148 | 28483679 (4287, 4288) | Novel Protein sim. GBank PROTEIN gi 1169207 sp P21705 DA82_YEAST - DAL82 | | UNCLASSIFIED | 1022 |
| 7149 | 20296427 (21059, 21060) | Novel Protein sim. GBank gi 1169271 sp P44948 FPG_HAEIN - FORMAMIDOPRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE) | | UNCLASSIFIED | 1034 |
| 7150 | 79238793 (295, 296) | Novel Protein sim. GBank gi 116983 sp P43574 GAT1_YEAST - GAT1 PROTEIN | | UNCLASSIFIED | 1003, 1008, 1017, 1022, 1026 |
| 7151 | 56026032 (18259, 18260) | Novel Protein sim. GBank gi 1169870 sp P46859 GC14_YEAST - GCD14 PROTEIN | | UNCLASSIFIED | 1008, 1009 |
| 7152 | 80080574 (22845, 22846) | Novel Protein sim. GBank gi 1170286 sp P44545 HFLC_HAEIN - HFLC PROTEIN | | UNCLASSIFIED | 1034 |
| 7153 | 11077845 (10793, 10794) | Novel Protein sim. GBank gi 1170356 sp P42270 HPCG_ECOLI - 2-OXO- HEPTA-3-ENE-1,7-DIOIC ACID HYDRATASE (OHD) HYDRATASE | | UNCLASSIFIED | 1024 |
| 7154 | 80232907 (18639, 18640) | Novel Protein sim. GBank gi 1170421 sp P46857 HUS2_YEAST - HUS2 PROTEIN | | UNCLASSIFIED | 1004, 1006, 1009, 1022 |
| 7155 | 65902299 (10709, 10710) | Novel Protein sim. GBank gi 1170500 sp P44323 IF2_HAEIN - TRANSLATION INITIATION FACTOR IF-2 | | UNCLASSIFIED | 1023 |
| 7156 | 85817675 (13327, 13328) | Novel Protein sim. GBank gi 1170546 sp P44851 ILVD_HAEIN - DIHYDROXY-ACID DEHYDRATASE (DAD) | | UNCLASSIFIED | 1019 |
| 7157 | 27367613 (19653, 19654) | Novel Protein sim. GBank gi 1170927 sp P45131 MET2_HAEIN - PUTATIVE HOMOSERINE O-ACETYLTRANSFERASE (HOMOSERINE O-TRANS-ACETYLASE) | | UNCLASSIFIED | 1017 |

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| 7158 5790) | 79111435 (5789, 5790) | Novel Protein sim. GBank g!11709501sp P43638 MHP1_YEAST - MAP- HOMOLOGOUS PROTEIN 1 | UNCLASSIFIED | 1022, 1023 |
| 7159 15966) | 27963648 (15965, 15966) | Novel Protein sim. GBank g!11709501sp P43638 MHP1_YEAST - MAP- HOMOLOGOUS PROTEIN 1 | UNCLASSIFIED | 1034 |
| 7160 4824) | 79598816 (4823, 4824) | Novel Protein sim. GBank g!11724471sp P43751 PFLA_HAEIN - PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME | UNCLASSIFIED | 1003 |
| 7161 22744) | 78407452 (22743, 22744) | Novel Protein sim. GBank g!11725091sp P42257 PILJ_PSEAE - PILJ PROTEIN | UNCLASSIFIED | 1006 |
| 7162 12166) | 28393442 (12165, 12166) | Novel Protein sim. GBank g!11725511sp P41812 POP1_YEAST - RNASES P/MRP PROTEIN POP1 | UNCLASSIFIED | 1008 |
| 7163 7262) | 20296014 (7261, 7262) | Novel Protein sim. GBank g!11727661sp P80210 PUR4_YEAST - ADENYLOSUCINATE SYNTHETASE (IMP- ASPARTATE LIGASE) | UNCLASSIFIED | 1034 |
| 7164 19478) | 80065593 (19477, 19478) | Novel Protein sim. GBank g!11727661sp P80210 PUR4_YEAST - ADENYLOSUCINATE SYNTHETASE (IMP- ASPARTATE LIGASE) | UNCLASSIFIED | 1003, 1004, 1006, 1017, 1039 |
| 7165 19932) | 80503242 (19931, 19932) | Novel Protein sim. GBank g!11728031sp P43123 QR1_YEAST - HYPOTHETICAL 53.5 KD PROTEIN IN PHO- POL3 INTERGENIC REGION | UNCLASSIFIED | 1012 |
| 7166 1126) | 80218225 (1125, 1126) | Novel Protein sim. GBank g!11728041sp P43124 QR12_YEAST - HYPOTHETICAL 46.1 KD PROTEIN IN PHO- POL3 INTERGENIC REGION | UNCLASSIFIED | 1004, 1006, 1010, 1017, 1022, 1026, 1034, 1038, 1044 |
| 7167 19036) | 5280127 (19035, 19036) | Novel Protein sim. GBank g!1172891sp P4886 CPT2_RAT - MITOCHONDRIAL CARNITINE O- PALMITOYLTRANSFERASE II PRECURSOR (CPT II) | UNCLASSIFIED | 1058 |

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| 7168 22710) | 71108523 (22709, Novel Protein sim. GBank g 1173039 sp P42766 RL35_HUMAN - 60S RIBOSOMAL PROTEIN L35 | | UNCLASSIFIED | 1029, 1046 |
| 7169 29683199 (625, 626) | Novel Protein sim. GBank g 1173375 sp P45978 SCD6_YEAST - SCD6 PROTEIN | | UNCLASSIFIED | 1009 |
| 7170 32548188 (13901, 13902) | Novel Protein sim. GBank g 1173451 sp P11994 SM50_STRPU - 50 KD SPICULE MATRIX PROTEIN PRECURSOR | | UNCLASSIFIED | 1006 |
| 7171 49522032 (17851, 17852) | Novel Protein sim. GBank g 1174092 U43360 - reverse transcriptase [Peromyscus maniculatus] | | UNCLASSIFIED | 1040 |
| 7172 87447974 (15987, 15988) | Novel Protein sim. GBank g 1174160 U44130 - p58 [Xenopus laevis] | | UNCLASSIFIED | 1025 |
| 7173 27968140 (19903, 19904) | Novel Protein sim. GBank g 1174538 sp P43831 SYQ_HAEIN - GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--T RNA LIGASE) (GLNRS) | | UNCLASSIFIED | 1006 |
| 7174 13086487 (20345, 20346) | Novel Protein sim. GBank g 11746611 sp P44594 TGT_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA- GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) | | UNCLASSIFIED | 1027, 1031 |
| 7175 77520895 (20251, 20252) | Novel Protein sim. GBank g 1174934 sp P44042 VACJ_HAEIN - VACJ LIPOPROTEIN HOMOLOG PRECURSOR | | UNCLASSIFIED | 1049 |
| 7176 79639238 (11427, 11428) | Novel Protein sim. GBank g 1175321 sp P44917 Y883_HAEIN - HYPOTHETICAL PROTEIN H10883 | | UNCLASSIFIED | 1038 |
| 7177 30168195 (8481, 8482) | Novel Protein sim. GBank g 1175468 sp Q09800 YAA7_SCHPO - HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I | | UNCLASSIFIED | 1030 |
| 7178 79180227 (18737, 18738) | Novel Protein sim. GBank g 1175542 sp P44123 YB90_HAEIN - HYPOTHETICAL PROTEIN H1190 | | UNCLASSIFIED | 1022, 1031 |

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| 7179 10163952 (13035, 13036) | Novel Protein sim. GBank g 1175687 sp P44732 ORDL_HAEIN - PROBABLE OXIDOREDUCTASE ORDL | UNCLASSIFIED | 1003 |
| 7180 30656662 (3149, 3150) | Novel Protein sim. GBank g 1175772 sp P45244 YDJA_HAEIN - HYPOTHETICAL PROTEIN HI1542 | UNCLASSIFIED | 1026 |
| 7181 78741684 (13913, 13914) | Novel Protein sim. GBank g 1175777 sp P44176 YCV_HAEIN - HYPOTHETICAL PROTEIN HI1400 | UNCLASSIFIED | 1008, 1039 |
| 7182 17936929 (1761, 1762) | Novel Protein sim. GBank g 1175779 sp P44189 YE18_HAEIN - HYPOTHETICAL PROTEIN HI1418 | UNCLASSIFIED | 1008, 1031 |
| 7183 25310980 (15681, 15682) | Novel Protein sim. GBank g 1175890 sp P44250 YCFW_HAEIN - HYPOTHETICAL PROTEIN HI1548 | UNCLASSIFIED | 1003 |
| 7184 79875270 (6713, 6714) | Novel Protein sim. GBank g 1175934 sp P43571 YFC5_YEAST - HYPOTHETICAL 117.8 KD PROTEIN IN STE2- FRS2 INTERGENIC REGION | UNCLASSIFIED | 1001, 1003, 1027 |
| 7185 78676588 (4449, 4450) | Novel Protein sim. GBank g 1175939 sp P43567 YFD0_YEAST - HYPOTHETICAL 41.9 KD PROTEIN IN HAC1- CAK1 INTERGENIC REGION | UNCLASSIFIED | 1017 |
| 7186 39547846 (2439, 2440) | Novel Protein sim. GBank g 1175940 sp P43566 YFD2_YEAST - HYPOTHETICAL 12.4 KD PROTEIN IN RIM15- HAC1 INTERGENIC REGION | UNCLASSIFIED | 1006 |
| 7187 27356171 (1747, 1748) | Novel Protein sim. GBank g 1175989 sp P43597 YF16_YEAST - HYPOTHETICAL 137.7 KD PROTEIN IN UGS1- FAB1 INTERGENIC REGION | UNCLASSIFIED | 1026 |
| 7188 56651079 (14131, 14132) | Novel Protein sim. GBank g 1176004 sp P43603 YF4_YEAST - HYPOTHETICAL 40.4 KD PROTEIN IN PES4- HIS2 INTERGENIC REGION | UNCLASSIFIED | 1003, 1008, 1009, 1022, 1026 |

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| 7189 | 20746548 (6611, 6612) | Novel Protein sim. GBank gi 1176008 sp P43605 YFJ7_YEAST - HYPOTHETICAL 31.8 KD PROTEIN IN HIS2- CDC14 INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 7190 | 80435774 (14817, 14818) | Novel Protein sim. GBank gi 1176008 sp P44568 RIMM_HAEIN - 16S RRNA PROCESSING PROTEIN RIMM | | UNCLASSIFIED | 1038 |
| 7191 | 56317997 (13421, 13422) | Novel Protein sim. GBank gi 1176046 sp P44278 YG26_HAEIN - HYPOTHETICAL PROTEIN H1626 | | UNCLASSIFIED | 1022 |
| 7192 | 20466513 (7007, 7008) | Novel Protein sim. GBank gi 1176050 sp P42937 YG4E_YEAST - HYPOTHETICAL 17.2 KD PROTEIN IN PCT1- ADE3 INTERGENIC REGION | | UNCLASSIFIED | 1010 |
| 7193 | 78759653 (16413, 16414) | Novel Protein sim. GBank gi 1176074 sp P46949 YG4A_YEAST - HYPOTHETICAL 90.8 KD PROTEIN IN RRP41- SNG1 INTERGENIC REGION | | UNCLASSIFIED | 1017 |
| 7194 | 79761150 (19941, 19942) | Novel Protein sim. GBank gi 1176281 sp P46852 YHHW_ECOLI - HYPOTHETICAL 26.3 KD PROTEIN IN GNTR- GGT INTERGENIC REGION (F231) | | UNCLASSIFIED | 1008 |
| 7195 | 80234391 (22605, 22606) | Novel Protein sim. GBank gi 1176338 sp P40355 YJ31_YEAST - HYPOTHETICAL 108.4 KD PROTEIN IN CBF1- NTA1 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1004, 1006, 1016, 1022 |
| 7196 | 13504992 (11759, 11760) | Novel Protein sim. GBank gi 1176356 sp P47039 YJG0_YEAST - HYPOTHETICAL AMINOTRANSFERASE YJL060W | | UNCLASSIFIED | 1004 |
| 7197 | 80099680 (11999, 12000) | Novel Protein sim. GBank gi 1176475 sp P40358 YJH3_YEAST - HYPOTHETICAL 80.4 KD PROTEIN IN SMC3- MRPL8 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1017, 1034 |
| 7198 | 11087395 (1309, 1310) | Novel Protein sim. GBank gi 1176480 sp P44453 YJT_HAEIN - HYPOTHETICAL PROTEIN H10012 | | UNCLASSIFIED | 1004 |

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| 7199 20604) | Novel Protein sim. GBank gil1176489 sp P42945 YJK9_YEAST - HYPOTHETICAL 200.0 KD PROTEIN IN GZF3- IME2 INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 7200 29457799 (1865, 1866) | Novel Protein sim. GBank gil1176580 sp P42836 YN66_YEAST - HYPOTHETICAL 39.2 KD PROTEIN IN EG72- KRE1 INTERGENIC REGION | | UNCLASSIFIED | 1009 |
| 7201 79174739 (22571, 22572) | Novel Protein sim. GBank gil1176580 sp P42836 YN66_YEAST - HYPOTHETICAL 39.2 KD PROTEIN IN EG72- KRE1 INTERGENIC REGION | | UNCLASSIFIED | 1024, 1026 |
| 7202 27837785 (15707, 15708) | Novel Protein sim. GBank gil1176586 sp P42842 YN53_YEAST - HYPOTHETICAL 102.3 KD PROTEIN IN DAL82- RFA2 INTERGENIC REGION | | UNCLASSIFIED | 1006 |
| 7203 80212686 (4505, 4506) | Novel Protein sim. GBank gil1176623 sp P41846 YO96_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III | | UNCLASSIFIED | 1044 |
| 7204 24133335 (1923, 1924) | Novel Protein sim. GBank gil1176823 sp P4530 IYRAP_HAEIN - HYPOTHETICAL PROTEIN HI1658 PRECURSOR | | UNCLASSIFIED | 1003, 1023 |
| 7205 11397882 (17423, 17424) | Novel Protein sim. GBank gil1176909 sp Q09625 YS8A_CAEEL - HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II | | UNCLASSIFIED | 1006 |
| 7206 80190649 (14477, 14478) | Novel Protein sim. GBank gil1176918 sp P24089 YSY2_YEAST - HYPOTHETICAL 137.7 KD PROTEIN IN SUBTELOMERIC Y' REPEAT REGION OF CHR XV (ORF 2) | | UNCLASSIFIED | 1004, 1006, 1008, 1009, 1022, 1024, 1029, 1034, 1038, 1058 |
| 7207 30652882 (20641, 20642) | Novel Protein sim. GBank gil1176986 sp P42413 OLB_BACSU - IOLB PROTEIN | | UNCLASSIFIED | 1022 |

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| 7208 20962) | 27830775 (20961, Novel Protein sim. GBank gi 1176986 sp P42413 OLB_BACSU - IOLB PROTEIN | | UNCLASSIFIED | 1004 |
| 7209 80256730 (14165, 14166) | Novel Protein sim. GBank gi 1181619 dbj BAA11565 - (D82364) a variant of TSC-22 [Gallus gallus] | | UNCLASSIFIED | 1022, 1034, 1037 |
| 7210 79444180 (16127, 16128) | Novel Protein sim. GBank gi 1181619 dbj BAA11565 - (D82364) a variant of TSC-22 [Gallus gallus] | | UNCLASSIFIED | 1022, 1030, 1034, 1040 |
| 7211 20432745 (5255, 5256) | Novel Protein sim. GBank gi 118302 sp P09890 DCDA_CORGL - DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE) | | UNCLASSIFIED | 1024 |
| 7212 99417275 (12469, 12470) | Novel Protein sim. GBank gi 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN | | UNCLASSIFIED | 1001, 1004, 1017, 1025, 1029, 1034, 1037, 1038, 1054 |
| 7213 80039105 (2187, 2188) | Novel Protein sim. GBank gi 119111 sp P12978 EBN2_EBV - EBNA-2 NUCLEAR PROTEIN | | UNCLASSIFIED | 1037, 1058 |
| 7214 94294597 (8853, 8854) | Novel Protein sim. GBank gi 119168 sp P09445 EF2_CRIGR - ELONGATION FACTOR 2 (EF-2) | | UNCLASSIFIED | 1024, 1026 |
| 7215 65484411 (4887, 4888) | Novel Protein sim. GBank gi 119712 sp P14918 EXTN_MAIZE - EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN) | | UNCLASSIFIED | 1038 |
| 7216 79763392 (1897, 1898) | Novel Protein sim. GBank gi 121058 sp P12754 E2BD_YEAST - TRANSLATION INITIATION FACTOR EIF-2B DELTA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCD2) (GCD COMPLEX SUBUNIT GCD2) | | UNCLASSIFIED | 1023 |

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| 7217 | 87892844 (11937, 11938) | Novel Protein sim. GBank g 121472 sp P04706 GLU2_MAIZE - GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) | UNCLASSIFIED | 1007, 1017, 1023, 1025, 1039 |
| 7218 | 11391492 (449, 450) | Novel Protein sim. GBank g 123330 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1010 |
| 7219 | 79444757 (2145, 2146) | Novel Protein sim. GBank g 123330 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1034 |
| 7220 | 11594422 (2699, 2700) | Novel Protein sim. GBank g 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1022 |
| 7221 | 79436235 (3639, 3640) | Novel Protein sim. GBank g 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1006 |
| 7222 | 28380726 (4207, 4208) | Novel Protein sim. GBank g 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1008 |
| 7223 | 11616471 (5917, 5918) | Novel Protein sim. GBank g 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1024 |
| 7224 | 11614608 (6171, 6172) | Novel Protein sim. GBank g 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1024 |
| 7225 | 80402888 (6533, 6534) | Novel Protein sim. GBank g 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | UNCLASSIFIED | 1010, 1029, 1034 |

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| 7226 | 46772992 (6635, 6636) | Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1042 |
| 7227 | 79444618 (10919, 10920) | Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1022 |
| 7228 | 95292713 (11687, 11688) | Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1010, 1024 |
| 7229 | 11399702 (14119, 14120) | Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR. | | UNCLASSIFIED | 1022 |
| 7230 | 85176113 (14955, 14956) | Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1034 |
| 7231 | 11613962 (15533, 15534) | Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1024 |
| 7232 | 79440943 (19479, 19480) | Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1024 |
| 7233 | 19539975 (20555, 20556) | Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1010 |
| 7234 | 79440440 (21049, 21050) | Novel Protein sim. GBank gil123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1010 |

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| 7235 21706) | 91226916 (21705, Novel Protein sim. GBank g 123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1010 |
| 7236 17902942 (22671, 22672) | Novel Protein sim. GBank g 123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1025 |
| 7237 13506251 (22925, 22926) | Novel Protein sim. GBank g 123530 sp P04929 HRPX_PLALO - HISTIDINE- RICH GLYCOPROTEIN PRECURSOR | | UNCLASSIFIED | 1034 |
| 7238 9535094 (2543, 2544) | Novel Protein sim. GBank g 125388 sp P223 3 KHR1_YEAST - KILLER TOXIN KHR PRECURSOR (KILLER OF HEAT RESISTANT) | | UNCLASSIFIED | 1006 |
| 7239 16304862 (5891, 5892) | Novel Protein sim. GBank g 125388 sp P223 3 KHR1_YEAST - KILLER TOXIN KHR PRECURSOR (KILLER OF HEAT RESISTANT) | | UNCLASSIFIED | 1024 |
| 7240 55007200 (13511, 13512) | Novel Protein sim. GBank g 126295 sp P08547 LIN1_HUMAN - LINE-1 REVERSE TRANSCRIPTASE HOMOLOG | | UNCLASSIFIED | 1019 |
| 7241 39520725 (21799, 21800) | Novel Protein sim. GBank g 126295 sp P08547 LIN1_HUMAN - LINE-1 REVERSE TRANSCRIPTASE HOMOLOG | | UNCLASSIFIED | 1010 |
| 7242 11100579 (22261, 22262) | Novel Protein sim. GBank g 126662 sp P253 0 LYCM_STRGL - LYSOZYME M1 PRECURSOR (1,4-BETA-N- ACETYL-MURAMIDASE M1) | | UNCLASSIFIED | 1006 |
| 7243 66490095 (14335, 14336) | Novel Protein sim. GBank g 126725 sp P211 39 MAN1_RAT - ALPHA- MANNOSIDASE (ALPHA-D-MANNOSIDE MANNOHYDROLASE) | | UNCLASSIFIED | 1010, 1029 |

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| 7244 | 17898280 (2465, 2486) | Novel Protein sim. GBank gi 126923 sp P22412 MDP1_PIG - MICROSSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP) | | |
| 7245 | 9882729 (11903, 11904) | Novel Protein sim. GBank gi 126980 sp P16523 MER1_YEAST - MEIOTIC RECOMBINATION 1 PROTEIN | UNCLASSIFIED | 1008 |
| 7246 | 80237292 (9585, 9586) | Novel Protein sim. GBank gi 127028 sp P15807 MET8_YEAST - MET8 PROTEIN | UNCLASSIFIED | 1006, 1008, 1024, 1034, 1054 |
| 7247 | 80238451 (12975, 12976) | Novel Protein sim. GBank gi 127091 sp P27705 MIG1_YEAST - REGULATORY PROTEIN MIG1 (REGULATOR PROTEIN CAT4) | UNCLASSIFIED | 1006, 1008, 1010, 1022, 1023, 1024, 1031 |
| 7248 | 97989906 (13185, 13186) | Novel Protein sim. GBank gi 128399 sp P14743 NMT_YEAST - GLYCYL PEPTIDE N-TETRADECANOYL TRANSFERASE (PEPTIDE N-MYristoyltransferase) (MYRISTOYL COA:PROTEIN N-MYRISTOYLTRANSFERASE) (NMT) | UNCLASSIFIED | 1004, 1008, 1009, 1010, 1022, 1024, 1025, 1026, 1031, 1038 |
| 7249 | 35933517 (17737, 17738) | Novel Protein sim. GBank gi 128853 sp P25284 NUEM_NEUCR - NADH-UBIQUINONE OXIDOREDUCTASE 40 KD SUBUNIT PRECURSOR (COMPLEX I-40KD) (CI-40KD) | UNCLASSIFIED | 1053 |
| 7250 | 78764791 (4289, 4290) | Novel Protein sim. GBank gi 1293734 U55021 - O3635p [Saccharomyces cerevisiae] | UNCLASSIFIED | 1003, 1044 |
| 7251 | 99393009 (13279, 13280) | Novel Protein sim. GBank gi 1293835 U56966 - C15H9.5 gene product [Caenorhabditis elegans] | UNCLASSIFIED | 1010, 1043 |
| 7252 | 80309285 (2785, 2786) | Novel Protein sim. GBank gi 129849 sp P10355 PT22_YEAST - PET122 PROTEIN PRECURSOR | UNCLASSIFIED | 1003, 1008, 1010, 1017, 1022, 1027, 1029, 1031 |

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| 7253 | 78780743 (20615) | Novel Protein sim. G-Bank g 130158 sp P05066 PHR_YEAST - DEOXYRIBODIPYRIMIDINE PHOTOLYASE PRECURSOR (DNA PHOTOLYASE) (PHOTOREACTIVATING ENZYME) | UNCLASSIFIED | 1009 |
| 7254 | 25139051 (3893, 3894) | Novel Protein sim. G-Bank g 130807 sp P19735 PR06_YEAST - PRE-mRNA SPLICING FACTOR PRP6 | UNCLASSIFIED | 1003, 1024 |
| 7255 | 78770835 (5673, 5674) | Novel Protein sim. G-Bank g 13089 sp P20457 PRI2_YEAST - DNA PRIMASE LARGE SUBUNIT (DNA PRIMASE 58 KD SUBUNIT) (P58) | UNCLASSIFIED | 1026, 1039 |
| 7256 | 57301086 (15045, 15046) | Novel Protein sim. G-Bank g 13142 sp P22356 PSPB_RAT - PULMONARY SURFACTANT-ASSOCIATED PROTEIN B PRECURSOR (SP-B) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SP1(PHE)) | UNCLASSIFIED | 1004, 1010, 1034 |
| 7257 | 10064064 (11539, 11540) | Novel Protein sim. G-Bank g 131490 sp P20966 PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-FRU) | UNCLASSIFIED | 1012 |
| 7258 | 87453399 (21053, 21054) | Novel Protein sim. G-Bank g 131605 sp P25822 PUM_DROME - MATERNAL PUMILIO PROTEIN | UNCLASSIFIED | 1025 |
| 7259 | 10094270 (11327, 11328) | Novel Protein sim. G-Bank g 131653 sp P25502 PUT3_YEAST - PROLINE UTILIZATION TRANS-ACTIVATOR | UNCLASSIFIED | 1038 |
| 7260 | 85525890 (11763, 11764) | Novel Protein sim. G-Bank g 132278 sp P03047 REGQ_LAMBD - ANTITERMINATION PROTEIN Q | UNCLASSIFIED | 1049 |

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| 7261 | 82782500 (1263, 1264) | Novel Protein sim. GBank gi 132339 sp P03872 REP2_YEAST - TRANS-ACTING FACTOR C (REP2) (PROTEIN CHARLIE) | | UNCLASSIFIED | 1044 |
| 7262 | 79860240 (1935, 1936) | Novel Protein sim. GBank gi 133144 sp P25299 RN15_YEAST - mRNA 3'-END PROCESSING PROTEIN RNA15 | | UNCLASSIFIED | 1017 |
| 7263 | 85531559 (16005, 16006) | Novel Protein sim. GBank gi 133520 emb CAA36480 - (X52235) ORFII [Homo sapiens] | | UNCLASSIFIED | 1038 |
| 7264 | 39586996 (749, 750) | Novel Protein sim. GBank gi 1339950 dbj BA12741 - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum] | | UNCLASSIFIED | 1006, 1024, 1034 |
| 7265 | 20633647 (2989, 2990) | Novel Protein sim. GBank gi 134196 sp P23832 SAMB_SALTY - SAMB PROTEIN | | UNCLASSIFIED | 1004 |
| 7266 | 80502023 (14377, 14378) | Novel Protein sim. GBank gi 13422 sp P20606 SAR1_YEAST - GTP-BINDING PROTEIN SAR1 | | UNCLASSIFIED | 1004, 1006, 1008, 1009, 1012, 1017, 1022, 1024, 1025, 1026, 1027, 1034, 1038, 1039, 1058 |
| 7267 | 38280077 (13529, 13530) | Novel Protein sim. GBank gi 134506 sp P06700 SIR2_YEAST - REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2) | | UNCLASSIFIED | 1008, 1022 |
| 7268 | 87453059 (19407, 19408) | Novel Protein sim. GBank gi 1346104 sp P49083 GBA1_ORYSA - GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT (GP-ALPHA-1) | | UNCLASSIFIED | 1025 |
| 7269 | 95198855 (2389, 2390) | Novel Protein sim. GBank gi 134634 sp P47135 JSN1_YEAST - JSN1 PROTEIN | | UNCLASSIFIED | 1008, 1029, 1044 |

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| 7270 | 57301782 (2929, 2930) | Novel Protein sim. GBank g!1346340 sp P47135 JSN1_YEAST - JSN1 PROTEIN | | UNCLASSIFIED | 1004, 1022, 1034 |
| 7271 | 28801598 (8563, 8564) | Novel Protein sim. GBank g!1346647 sp P49687 N145_YEAST - NUCLEOPORIN NUP145 (NUCLEAR PORE PROTEIN NUP145) | | UNCLASSIFIED | 1017, 1024 |
| 7272 | 80079596 (13885, 13886) | Novel Protein sim. GBank g!1346721 sp P49022 PIP_LACLA - PHAGE INFECTION PROTEIN | | UNCLASSIFIED | 1034 |
| 7273 | 11776932 (15913, 15914) | Novel Protein sim. GBank g!1346916 sp P12283 PJRA_ECOLI - ADENYLOSUCINATE SYNTHETASE (IMP-ASPARTATE LIGASE) | | UNCLASSIFIED | 1006 |
| 7274 | 29014276 (15647, 15648) | Novel Protein sim. GBank g!1347801 sp P14328 SP96_DICDI - SPORE COAT PROTEIN SP96 | | UNCLASSIFIED | 1030 |
| 7275 | 47654653 (18403, 18404) | Novel Protein sim. GBank g!1347601 sp P14328 SP96_DICDI - SPORE COAT PROTEIN SP96 | | UNCLASSIFIED | 1029, 1053 |
| 7276 | 65685543 (10481, 10482) | Novel Protein sim. GBank g!134781 sp P23201 SPA2_YEAST - SPA2 PROTEIN | | UNCLASSIFIED | 1049 |
| 7277 | 81743047 (14507, 14508) | Novel Protein sim. GBank g!134853 sp P27692 SPT5_YEAST - TRANSCRIPTION INITIATION PROTEIN SPT5 | | UNCLASSIFIED | 1004, 1006, 1012, 1017, 1024, 1034, 1038, 1039, 1054 |
| 7278 | 65460683 (9065, 9066) | Novel Protein sim. GBank g!134854 sp P23615 SPT6_YEAST - TRANSCRIPTION INITIATION PROTEIN SPT6 | | UNCLASSIFIED | 1054 |
| 7279 | 78926555 (22527, 22528) | Novel Protein sim. GBank g!134856 sp P09139 SPYA_RAT - SERINE-PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (SPT) (ALANINE-GLYOXYLATE AMINOTRANSFERASE) (AGT) | | UNCLASSIFIED | 1008 |

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| 7280 | 82452137 (7861, 7862) | Novel Protein sim. GBank g 134935 sp P11972 SSST2 _YEAST - SST2 PROTEIN | | UNCLASSIFIED | 1001, 1004, 1006, 1008, 1010, 1012, 1017, 1021, 1022, 1023, 1024, 1031, 1034, 1038, 1039, 1044, 1054 |
| 7281 | 11077318 (6707, 6708) | Novel Protein sim. GBank g 135142 sp P26700 YPH_BPP2 - PROBABLE TAIL FIBRE PROTEIN (GPH) | | UNCLASSIFIED | 1004, 1008 |
| 7282 | 20458563 (1973, 19734) | Novel Protein sim. GBank g 135172 sp Q10110 YAQA_SCHPO - HYPOTHETICAL 88.6 KD PROTEIN C18G6.10C IN CHROMOSOME 1 | | UNCLASSIFIED | 1010 |
| 7283 | 39456271 (6425, 6426) | Novel Protein sim. GBank g 135175 sp P18255 SYT1_BACSU - THREONYL TRNA SYNTHETASE 1 (THREONINE-TRNA LIGASE) (THRRS) | | UNCLASSIFIED | 1006 |
| 7284 | 94666466 (6775, 6776) | Novel Protein sim. GBank g 135181 sp P48234 YG3J_YEAST - HYPOTHETICAL 81.7 KD PROTEIN IN MOL1- NAT2 INTERGENIC REGION | | UNCLASSIFIED | 1024, 1034 |
| 7285 | 27836711 (5477, 5478) | Novel Protein sim. GBank g 135182 sp P39927 YG3Q_YEAST - HYPOTHETICAL 47.0 KD PROTEIN IN CYS4- PEM1 INTERGENIC REGION | | UNCLASSIFIED | 1006 |
| 7286 | 78387082 (18149, 18150) | Novel Protein sim. GBank g 135283 sp P06921 VE2_HPV05 - REGULATORY PROTEIN E2 | | UNCLASSIFIED | 1026 |
| 7287 | 78778316 (20623, 20624) | Novel Protein sim. GBank g 135287 sp P47108 YJ11_YEAST - HYPOTHETICAL 135.1 KD PROTEIN IN GEF1- NUP85 INTERGENIC REGION | | UNCLASSIFIED | 1026 |

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| 7288 | 79831931 (1713, 1714) | Novel Protein sim. GBank g 1352880 sp P47110 YJ13_YEAST - HYPOTHETICAL 40.3 KD PROTEIN IN NUP85- SSC1 INTERGENIC REGION | | UNCLASSIFIED | 1008, 1022, 1044 |
| 7289 | 56470631 (13149, 13150) | Novel Protein sim. GBank g 1352890 sp P47123 YJ44_YEAST - HYPOTHETICAL 24.3 KD PROTEIN IN PEM2- HOC1 INTERGENIC REGION | | UNCLASSIFIED | 1017 |
| 7290 | 78896911 (15183, 15184) | Novel Protein sim. GBank g 1352911 sp P47147 YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2- NNF1 INTERGENIC REGION | | UNCLASSIFIED | 1017 |
| 7291 | 79113310 (19465, 19466) | Novel Protein sim. GBank g 1352911 sp P47147 YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2- NNF1 INTERGENIC REGION | | UNCLASSIFIED | 1003 |
| 7292 | 65442574 (1821, 1822) | Novel Protein sim. GBank g 1352912 sp P47148 YJ81_YEAST - HYPOTHETICAL 32.2 KD PROTEIN IN CPA2- NNF1 INTERGENIC REGION | | UNCLASSIFIED | 1049 |
| 7293 | 28794827 (993, 994) | Novel Protein sim. GBank g 1352936 sp P47171 YJ9H_YEAST - HYPOTHETICAL 191.7 KD PROTEIN IN HOM6- PMT4 INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 7294 | 17676882 (10381, 10382) | Novel Protein sim. GBank g 1352943 sp P47178 YJ9O_YEAST - HYPOTHETICAL 29.5 KD PROTEIN IN BAT2- DAL5 INTERGENIC REGION PRECURSOR | | UNCLASSIFIED | 1039 |
| 7295 | 78791899 (4659, 4860) | Novel Protein sim. GBank g 1352944 sp P47179 YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2- DAL5 INTERGENIC REGION PRECURSOR | | UNCLASSIFIED | 1009 |
| 7296 | 20696279 (18055, 18056) | Novel Protein sim. GBank g 1352952 sp P47080 YJA7_YEAST - HYPOTHETICAL 11.9 KD PROTEIN IN CCT8- CTK2 INTERGENIC REGION | | UNCLASSIFIED | 1006 |

| | | Novel Protein sim. GBank g 1352962 sp P47089 YJB9_YEAST - HYPOTHETICAL 72.4 KD PROTEIN IN PET130- CCT3 INTERGENIC REGION | UNCLASSIFIED | 1022 |
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| 7297 | 8498789 (11183, 11184) | Novel Protein sim. GBank g 1352981 sp P47046 YJF1_YEAST - HYPOTHETICAL 91.3 KD PROTEIN IN TDH1- MTR4 INTERGENIC REGION | UNCLASSIFIED | 1004 |
| 7298 | 20446403 (4639, 4640) | Novel Protein sim. GBank g 1352981 sp P47046 YJF1_YEAST - HYPOTHETICAL 91.3 KD PROTEIN IN TDH1- MTR4 INTERGENIC REGION | UNCLASSIFIED | 1004, 1016, 1024 |
| 7299 | 82114223 (659, 660) | Novel Protein sim. GBank g 1352995 sp P47031 YJ12_YEAST - HYPOTHETICAL 82.5 KD PROTEIN IN EXO70- ARP4 INTERGENIC REGION | UNCLASSIFIED | 1006 |
| 7300 | 79186760 (14717, 14718) | Novel Protein sim. GBank g 1352995 sp P47031 YJ12_YEAST - HYPOTHETICAL 82.5 KD PROTEIN IN EXO70- ARP4 INTERGENIC REGION | UNCLASSIFIED | 1017 |
| 7301 | 17894667 (847, 848) | Novel Protein sim. GBank g 1353043 sp P46982 YJS6_YEAST - HYPOTHETICAL 67.3 KD PROTEIN IN SWE1- ATP12 INTERGENIC REGION | UNCLASSIFIED | 1034 |
| 7302 | 30383911 (4599, 4600) | Novel Protein sim. GBank g 1353050 sp P47086 YJY1_YEAST - HYPOTHETICAL 30.5 KD PROTEIN IN SPC1- ILV3 INTERGENIC REGION | UNCLASSIFIED | 1003 |
| 7303 | 23295044 (4507, 4508) | Novel Protein sim. GBank g 1353083 sp P49017 COQ5_YEAST - UBIQUINONE BIOSYNTHESIS METHYLTRANSFERASE COQ5 | UNCLASSIFIED | 1009 |
| 7304 | 38277876 (8553, 8554) | Novel Protein sim. GBank g 1353105 sp P48563 YN37_YEAST - HYPOTHETICAL 186.8 KD PROTEIN IN CLA4- MID1 INTERGENIC REGION | UNCLASSIFIED | 1034 |
| 7305 | 20285552 (12003, 12004) | Novel Protein sim. GBank g 1361215 pir S56581 - methyl-accepting chemotaxis protein 1 - Escherichia coli | UNCLASSIFIED | |

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| 7306 | 79866035 (10433) 10434) | Novel Protein sim. GBank gil1363693 pir S58781 - probable membrane protein YDL196w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022, 1038 |
| 7307 | 78372416 (10739, 10740) | Novel Protein sim. GBank gil1363731 pir S59414 - hypothetical protein YLR455w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1039 |
| 7308 | 30642846 (7251, 7252) | Novel Protein sim. GBank gil1363748 pir S59408 - probable membrane protein YLR440c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 7309 | 30615264 (9405, 9406) | Novel Protein sim. GBank gil1363751 pir S59382 - hypothetical protein YLR417w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1009, 1026 |
| 7310 | 9884992 (18215, 18216) | Novel Protein sim. GBank gil138595 sp P02845 VIT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) (CONTAINS: LIPOVITELLIN I (LV); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40) | | UNCLASSIFIED | 1008 |
| 7311 | 10095761 (17109, 17110) | Novel Protein sim. GBank gil139232 sp P16753 VP40_HCMVA - CAPSID PROTEIN P40 (CONTAINS: ASSEMBLIN (PROTEASE) AND CAPSID ASSEMBLY PROTEIN) | | UNCLASSIFIED | 1038 |
| 7312 | 27929979 (20013, 20014) | Novel Protein sim. GBank gil139965 (U62317) - hypothetical protein 384D8_6 [Homo sapiens] | | UNCLASSIFIED | 1006, 1010 |
| 7313 | 20464958 (19943, 19944) | Novel Protein sim. GBank gil140025 sp P06557 DNA1_BACSU - PRIMOSOMAL PROTEIN DNA1 | | UNCLASSIFIED | 1010 |
| 7314 | 29342129 (7141, 7142) | Novel Protein sim. GBank gil140331 sp P25537 YCA5_YEAST - HYPOTHETICAL 28.7 KD PROTEIN IN CWH36-PEL1 INTERGENIC REGION | | UNCLASSIFIED | 1022 |

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| 7315 | 39547428 (14057, 14058) | Novel Protein sim. GBank gi 140332 sp P25555 YCA6_YEAST - HYPOTHETICAL 12.5 KD PROTEIN IN CWH36- PEL1 INTERGENIC REGION | UNCLASSIFIED | 1006 |
| 7316 | 9522648 (20733, 20734) | Novel Protein sim. GBank gi 140338 sp P21367 YCAC_ECOLI - HYPOTHETICAL 23.1 KD PROTEIN IN DMSC- PFLA INTERGENIC REGION | UNCLASSIFIED | 1003 |
| 7317 | 95293089 (3161, 3162) | Novel Protein sim. GBank gi 140351 sp P255384 YCB9_YEAST - TRANSPONSON TY1-17 PROTEIN B | UNCLASSIFIED | 1024 |
| 7318 | 27824104 (5711, 5712) | Novel Protein sim. GBank gi 140372 sp P25569 YCD9_YEAST - HYPOTHETICAL 86.0 KD PROTEIN IN GLK1- SRO9 INTERGENIC REGION | UNCLASSIFIED | 1024 |
| 7319 | 80478105 (22263, 22264) | Novel Protein sim. GBank gi 140372 sp P25569 YCD9_YEAST - HYPOTHETICAL 86.0 KD PROTEIN IN GLK1- SRO9 INTERGENIC REGION | UNCLASSIFIED | 1012, 1022 |
| 7320 | 17896104 (777, 778) | Novel Protein sim. GBank gi 140380 sp P25576 YCE7_YEAST - HYPOTHETICAL 29.7 KD PROTEIN IN APA1/DTP-PD11 INTERGENIC REGION | UNCLASSIFIED | 1044 |
| 7321 | 6756409 (4849, 4850) | Novel Protein sim. GBank gi 140477 sp P25533 YCR6_YEAST - HYPOTHETICAL 84.9 KD PROTEIN IN PMP1- FEN2 INTERGENIC REGION | UNCLASSIFIED | 1022 |
| 7322 | 95294802 (6763, 6764) | Novel Protein sim. GBank gi 140525 sp P25541 YCV8_YEAST - HYPOTHETICAL 49.3 KD PROTEIN IN SCC3 5REGION | UNCLASSIFIED | 1010, 1022, 1058 |
| 7323 | 25136226 (10049, 10050) | Novel Protein sim. GBank gi 140544 emb CAA66080.1 - (X97449) primosomal protein N [Borrelia burgdorferi] | UNCLASSIFIED | 1026 |

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| 7324 | 20598718 (15705, 15706) | Novel Protein sim. GBank g 140687 sp P11666 YGGB_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286) | UNCLASSIFIED | 1053 |
| 7325 | 20617110 (20331, 20332) | Novel Protein sim. GBank g 140723 sp P25439 HRCA_BACSU - HEAT- INDUCIBLE TRANSCRIPTION REPRESSOR HRCA. | UNCLASSIFIED | 1004 |
| 7326 | 9644134 (21117, 21118) | Novel Protein sim. GBank g 140750 sp P25536 YHDE_ECOLI - HYPOTHETICAL 21.5 KD PROTEIN IN CAFAB- MRED INTERGENIC REGION (ORFE) | UNCLASSIFIED | 1039 |
| 7327 | 21434980 (22405, 22406) | Novel Protein sim. GBank g 141103 sp P11260 YO11_MOUSE - HYPOTHETICAL PROTEIN ORF-1137 | UNCLASSIFIED | 1024 |
| 7328 | 78103835 (3243, 3244) | Novel Protein sim. GBank g 141470 sp P19658 EX70_YEAST - 70 KD EXOCYST COMPLEX PROTEIN | UNCLASSIFIED | 1036 |
| 7329 | 80234966 (14657, 14658) | Novel Protein sim. GBank g 141515 sp P25639 YCV1_YEAST - HYPOTHETICAL 65.0 KD PROTEIN IN PWP2- SUP61 INTERGENIC REGION | UNCLASSIFIED | 1001, 1003, 1016, 1022 |
| 7330 | 79830278 (3163, 3164) | Novel Protein sim. GBank g 1460074 emb CAB01049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1039, 1049 |
| 7331 | 19885057 (8677, 8678) | Novel Protein sim. GBank g 1460074 emb CAB01049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1001 |
| 7332 | 24125719 (13983, 13984) | Novel Protein sim. GBank g 1469982 dbj BAA09771 - (D63484) The KIAA0150 gene product is novel. [Homo sapiens] | UNCLASSIFIED | 1009 |
| 7333 | 79965185 (14059, 14060) | Novel Protein sim. GBank g 1497861 U40587 - fiber gene product [Fowl adenovirus] | UNCLASSIFIED | 1025 |

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| 7334 | 65472599 (903, 904) | Novel Protein sim. GBank gil1524205[emb CAB01993] - (Z79700) putH [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1010, 1023 |
| 7335 | 8488433 (12359, 12360) | Novel Protein sim. GBank gil1552873[emb CAB02469] - (Z80343) hypothetical protein RV3790 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1024 |
| 7336 | 16395807 (10211, 10212) | Novel Protein sim. GBank gil1572819 (U70855) - similar to the RAS gene family [Caenorhabditis elegans] | | UNCLASSIFIED | 1017 |
| 7337 | 78747341 (12127, 12128) | Novel Protein sim. GBank gil1573895 (U32769) - conserved hypothetical protein [Haemophilus influenzae Ra] | | UNCLASSIFIED | 1022 |
| 7338 | 88083418 (9847, 9848) | Novel Protein sim. GBank gil1622787 (U47644) - Notch2 gene product [Felina leukemia virus] | | UNCLASSIFIED | 1008, 1054 |
| 7339 | 78700638 (2697, 2698) | Novel Protein sim. GBank gil1644222[dbj BAA11082] - (D67066) N-WASP [Bos taurus] | | UNCLASSIFIED | 1017 |
| 7340 | 37003614 (2117, 2118) | Novel Protein sim. GBank gil1644457 (U72521) - neural variant mena+ protein [Mus musculus] | | UNCLASSIFIED | 1029 |
| 7341 | 78183445 (12563, 12564) | Novel Protein sim. GBank gil1648880[emb CAB03669] - (Z81331) hypothetical protein RV2840c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1029, 1053 |
| 7342 | 80069047 (3803, 3804) | Novel Protein sim. GBank gil1651952[dbj BAA16878] - (D90901) precorrin methylase [Synechocystis sp.] | | UNCLASSIFIED | 1010, 1023 |
| 7343 | 80500859 (4009, 4010) | Novel Protein sim. GBank gil1652206[dbj BAA17130] - (D90903) regulatory components of sensory transduction system [Synechocystis sp.] | | UNCLASSIFIED | 1006, 1012 |
| 7344 | 80050260 (14527, 14528) | Novel Protein sim. GBank gil1652750[dbj BAA17669] - (D90908) transcriptional regulator [Synechocystis sp.] | | UNCLASSIFIED | 1004 |
| 7345 | 37034601 (1467, 1468) | Novel Protein sim. GBank gil1652893[dbj BAA17811] - (D90909) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1012 |

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| 7346 | 88094359 (5937, 5938) | Novel Protein sim. GBank gi 1653184 dbj BAA18100 - (D90911) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1010 |
| 7347 | 32436128 (19103, 19104) | Novel Protein sim. GBank gi 1653325 dbj BAA18240 - (D90912) lymphocyte protein cThy28kD [Synechocystis sp.] | | UNCLASSIFIED | 1029 |
| 7348 | 82443430 (20183, 20184) | Novel Protein sim. GBank gi 1653805 dbj BAA18716 - (D90916) hypothetical protein [Synechocystis sp.] | | UNCLASSIFIED | 1001, 1012, 1022, 1023, 1034, 1044 |
| 7349 | 30858118 (5293, 5294) | Novel Protein sim. GBank gi 1654108 dbj BAA1283 - RpoE homologue [Rhodobacter sphaeroides] | | UNCLASSIFIED | 1026 |
| 7350 | 20619990 (5613, 5614) | Novel Protein sim. GBank gi 1655665 emb CAB03731 - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1004, 1024 |
| 7351 | 95002716 (10637, 10638) | Novel Protein sim. GBank gi 1655669 emb CAA68032 - (Y07752) pherophorin-S [Volvox carteri] | | UNCLASSIFIED | 1006 |
| 7352 | 70950672 (17639, 17640) | Novel Protein sim. GBank gi 1655669 emb CAA68032 - (Y07752) pherophorin-S [Volvox carteri] | | UNCLASSIFIED | 1029 |
| 7353 | 25255880 (17699, 17700) | Novel Protein sim. GBank gi 1657608 dbj BAA13405 - (D87466) orf5 [Streptococcus pneumoniae] | | UNCLASSIFIED | 1008 |
| 7354 | 78743353 (4549, 4550) | Novel Protein sim. GBank gi 1665817 dbj BAA13405 - (D87466) Similar to S. cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens] | | UNCLASSIFIED | 1025, 1044 |
| 7355 | 18552821 (2487, 2488) | Novel Protein sim. GBank gi 1666137 emb CAB05053 - (Z82098) hypothetical protein Rv3523 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1001 |
| 7356 | 78674147 (16331, 16332) | Novel Protein sim. GBank gi 1666689 dbj BAA13405 - (D87466) alpha-NAC, muscle-specific form gp220 [Mus musculus] | | UNCLASSIFIED | 1026 |
| 7357 | 37797730 (17479, 17480) | Novel Protein sim. GBank gi 1673402 emb CAB04812 - (Z82044) hypothetical 54.4 kd protein [Bacillus subtilis] | | UNCLASSIFIED | 1012 |

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| 7358 15870) | 78707254 (15869, Novel Protein sim. GBank qj11679692 (U76205) - scavenger receptor class B type I [Rattus norvegicus] | | UNCLASSIFIED | 1008, 1022, 1026, 1039 |
| 7359 80054196 (14549, 14550) | Novel Protein sim. GBank qj116841738 emb CAJ706011 - (Y09452) Yed j hypothetical protein [Pseudomonas syringae] | | UNCLASSIFIED | 1004, 1024 |
| 7360 7533261 (2819, 2820) | Novel Protein sim. GBank qj11688307 (U78556) - disulfatase resistance associated alpha protein [Homo sapiens] | | UNCLASSIFIED | 1058 |
| 7361 80082471 (15365, 15366) | Novel Protein sim. GBank qj11694359 emb CAB05439 - (Z83018) hypothetical protein RV2972c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1034 |
| 7362 37392439 (5241, 5242) | Novel Protein sim. GBank qj11703228 sp P52893 ALAM_YEAST - PUTATIVE ALANINE AMINO-TRANSFERASE, MITOCHONDRIAL PRECURSOR (GLUTAMIC- PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC- ALANINE TRANSAMINASE) | | UNCLASSIFIED | 1003, 1036 |
| 7363 79112104 (20729, 20730) | Novel Protein sim. GBank qj11703440 sp P50275 ASE1_YEAST - ANAPHASE SPINDLE ELONGATION PROTEIN | | UNCLASSIFIED | 1017, 1039 |
| 7364 54530976 (1, 2) | Novel Protein sim. GBank qj11705513 sp P47136 BUD4_YEAST - BUD SITE SELECTION PROTEIN BUD4 | | UNCLASSIFIED | 1041 |
| 7365 17649323 (22135, 22136) | Novel Protein sim. GBank qj11706001 sp P32074 COPG_YEAST - COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP) | | UNCLASSIFIED | 1017 |
| 7366 17295570 (7379, 7380) | Novel Protein sim. GBank qj11706711 sp P53573 ETFA_BRAJA - ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT (ALPHA-ETF) (ELECTRON TRANSFER FLAVOPROTEIN LARGE SUBUNIT) (ETFLS) | | UNCLASSIFIED | 1039 |

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| 7367 | 27959424 (5985, 5986) | Novel Protein sim. GBank PROTEIN gi 1706879 sp P50264 FMS1_YEAST - FMS1 | | UNCLASSIFIED | 1006 |
| 7368 | 20740759 (1103, 1104) | Novel Protein sim. GBank gi 1706929 sp Q10989 FTSY_MYCTU - CELL DIVISION PROTEIN FTSY HOMOLOG | | UNCLASSIFIED | 1001, 1022 |
| 7369 | 85216550 (6381, 6382) | Novel Protein sim. GBank gi 1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE_8F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8.... | | UNCLASSIFIED | 1010 |
| 7370 | 21422954 (10085, 10086) | Novel Protein sim. GBank gi 1707713 emb CAA69507 - (Y08256) orf cd6024 [Sulfolobus solfataricus] | | UNCLASSIFIED | 1022, 1024, 1027, 1034 |
| 7371 | 80481749 (7733, 7734) | Novel Protein sim. GBank gi 1707970 sp Q10379 GLNE_MYCTU - PROBABLE GLUTAMATE-AMMONIA-LIGASE ADENYLYLTRANSFERASE (GLUTAMINE- SYNTHETASE ADENYLYLTRANSFERASE) (ATASE) | | UNCLASSIFIED | 1006, 1010, 1012, 1024, 1026 |
| 7372 | 79954868 (3983, 3984) | Novel Protein sim. GBank gi 1708869 sp P52691 LRRKA_SYNPT7 - PROBABLE TRANSCRIPTIONAL REGULATOR LRRKA | | UNCLASSIFIED | 1001 |
| 7373 | 1304695 (12565, 12566) | Novel Protein sim. GBank gi 1708874 sp P52689 LTRA_KLEPN - PROBABLE TRANSCRIPTIONAL REGULATOR LTRA | | UNCLASSIFIED | 1024 |
| 7374 | 78469078 (19997, 19998) | Novel Protein sim. GBank gi 1709285 sp P52965 NIFJ_SYNY3 - PUTATIVE PYRUVATE-FLAVODOXIN OXIDOREDUCTASE | | UNCLASSIFIED | 1026 |
| 7375 | 80026646 (10841, 10842) | Novel Protein sim. GBank gi 1709621 sp P51533 PDR_A_YEAST - ATP- DEPENDENT PERMEASE PDR10 | | UNCLASSIFIED | 1004, 1006, 1017 |

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| 7376 | 11090572 (4213, 4214) | Novel Protein sim. GBank gi 1709733 sp P51065 PPCK_STAAU - PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) | | UNCLASSIFIED | 1006 |
| 7377 | 79888025 (12483, 12484) | Novel Protein sim. GBank gi 1709751 sp P55174 PQQF_PSEFL - COENZYME PQQ SYNTHESIS PROTEIN F | | UNCLASSIFIED | 1003 |
| 7378 | 8500276 (22941, 22942) | Novel Protein sim. GBank gi 1709753 sp P32523 PR19_YEAST - PRE-MRNA SPLICING FACTOR PRP19 | | UNCLASSIFIED | 1004 |
| 7379 | 13041977 (7213, 7214) | Novel Protein sim. GBank gi 1710106 sp Q10606 RFE_MYCTU - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE | | UNCLASSIFIED | 1024 |
| 7380 | 32297376 (14083, 14084) | Novel Protein sim. GBank gi 1710216 (U79260) - Unknown [Homo sapiens] | | UNCLASSIFIED | 1000 |
| 7381 | 80077389 (9745, 9746) | Novel Protein sim. GBank gi 1710383 sp P46352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX | | UNCLASSIFIED | 1034 |
| 7382 | 80223293 (773, 774) | Novel Protein sim. GBank gi 1711345 sp P53012 SCS3_YEAST - SCS3 PROTEIN | | UNCLASSIFIED | 1003, 1008, 1024, 1031 |
| 7383 | 29347374 (1133, 1134) | Novel Protein sim. GBank gi 1711392 sp P06701 SIR3_YEAST - REGULATORY PROTEIN SIR3(SILENT INFORMATION REGULATOR 3) | | UNCLASSIFIED | 1022 |
| 7384 | 20731350 (18963, 18964) | Novel Protein sim. GBank gi 1711396 sp P54867 SLG1_YEAST - SLG1 PROTEIN PRECURSOR | | UNCLASSIFIED | 1004 |
| 7385 | 80504082 (9335, 9336) | Novel Protein sim. GBank gi 1711489 sp P54988 SOXC_RHOSO - DIBENZOTIOPHENE DESULFURIZATION ENZYME C (DBT SULFUR DIOXYGENASE) | | UNCLASSIFIED | 1012 |

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| 7386 | 80503589 (15415, 15416) | Novel Protein sim. GBank g 1711497 sp P53541 SPO1_YEAST - SPORULATION PROTEIN SPO1 | | UNCLASSIFIED | 1006, 1008, 1012, 1022, 1024 |
| 7387 | 79831391 (20455, 20456) | Novel Protein sim. GBank g 1711619 sp P53628 SNFC_YEAST - TRANSCRIPTION REGULATORY PROTEIN SNF12 (SWI/SNF COMPLEX COMPONENT SWP73) | | UNCLASSIFIED | 1008, 1024 |
| 7388 | 78788083 (9721, 9722) | Novel Protein sim. GBank g 171374 (M60415) - DAL81 [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1009, 1022 |
| 7389 | 29203926 (8325, 8326) | Novel Protein sim. GBank g 171483 (M59708) - sec21D [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1008 |
| 7390 | 27842655 (6667, 6668) | Novel Protein sim. GBank g 171596 (J04719) - D- fructose-6-phosphate amidotransferase (EC 2.6.1.16) [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1006 |
| 7391 | 10224420 (6703, 6704) | Novel Protein sim. GBank g 171666 (M33703) - Hex2_protein [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1022, 1034 |
| 7392 | 20625793 (18135, 18136) | Novel Protein sim. GBank g 171940 (M84455) - leucine zipper protein [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1023, 1034 |
| 7393 | 30658154 (11121, 11122) | Novel Protein sim. GBank g 172076 (M88605) - contains Cys-4 zinc-finger, resembles erythroid- transcription factor GATA-1; ORF [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1026 |
| 7394 | 11135839 (13607, 13608) | Novel Protein sim. GBank g 172081 (M88607) - H1-like protein, high in lys and ser; ORF 2 [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1034 |
| 7395 | 79564830 (16607, 16608) | Novel Protein sim. GBank g 172094 (M36822) - SIN3 open reading frame [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1001, 1008, 1022 |
| 7396 | 7431475 (2059, 2060) | Novel Protein sim. GBank g 172096 (M90688) - polyA nuclease [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1058 |
| 7397 | 78459988 (6569, 6570) | Novel Protein sim. GBank g 1723026 sp Q10897 Y05L_MYCTU - HYPOTHETICAL 70.4 KD PROTEIN CY251.21 | | UNCLASSIFIED | 1026 |

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| 7398 | 20370183 (13393, 13394) | Novel Protein sim. GBank g 1723119 sp P53890 Y174_HUMAN - HYPOTHETICAL PROTEIN_KIAA0174 | | UNCLASSIFIED | 1024 |
| 7399 | 78770076 (20677, 20678) | Novel Protein sim. GBank g 1723183 sp P39734 YAC8_YEAST - HYPOTHETICAL 58.8 KD PROTEIN IN MYO4- DRS2 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1017, 1034, 1039, 1044 |
| 7400 | 10206877 (16945, 16946) | Novel Protein sim. GBank g 1723189 sp P39731 YADA_YEAST - HYPOTHETICAL 33.2 KD PROTEIN IN PYK1- SNC1 INTERGENIC REGION | | UNCLASSIFIED | 1025 |
| 7401 | 86685530 (13541, 13542) | Novel Protein sim. GBank g 1723279 sp Q10211 YAY3_SC1HPO - HYPOTHETICAL 74.5 KD PROTEIN C4H3.03C IN CHROMOSOME 1 | | UNCLASSIFIED | 1029 |
| 7402 | 78899607 (16101, 16102) | Novel Protein sim. GBank g 1723566 sp Q10479 YDF7_SC1HPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07 | | UNCLASSIFIED | 1017 |
| 7403 | 80216490 (20481, 20482) | Novel Protein sim. GBank g 1723647 sp P53209 YG1A_YEAST - HYPOTHETICAL 22.2 KD PROTEIN IN MSB2- UGA1 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1004, 1006, 1009, 1010, 1017, 1022, 1024, 1034 |
| 7404 | 27823645 (6791, 6792) | Novel Protein sim. GBank g 1723669 sp P53235 YG22_YEAST - HYPOTHETICAL 71.3 KD PROTEIN IN SCM4- MUP1 INTERGENIC REGION | | UNCLASSIFIED | 1024 |
| 7405 | 5602652 (8819, 8820) | Novel Protein sim. GBank g 1723688 sp P53255 YG2M_YEAST - HYPOTHETICAL 58.2 KD PROTEIN IN DBF2- VAS1 INTERGENIC REGION | | UNCLASSIFIED | 1058 |
| 7406 | 79775783 (893, 894) | Novel Protein sim. GBank g 1723691 sp P53259 YG2Q_YEAST - HYPOTHETICAL 38.8 KD PROTEIN IN MIC1- SRB5 INTERGENIC REGION | | UNCLASSIFIED | 1008, 1017 |

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| 7407 | 11084202 (6749, 6750) | Novel Protein sim. GBank g 1723693 sp P53261 YG2S_YEAST - HYPOTHETICAL 69.9 KD PROTEIN IN M1C1- SRB5 INTERGENIC REGION | UNCLASSIFIED | 1024 |
| 7408 | 79629257 (9199, 9200) | Novel Protein sim. GBank g 1723697 sp P53265 YG2W_YEAST - HYPOTHETICAL 46.7 KD PROTEIN IN CLB6- SPT6 INTERGENIC REGION | UNCLASSIFIED | 1025 |
| 7409 | 39548985 (18627, 18628) | Novel Protein sim. GBank g 1723697 sp P53265 YG2W_YEAST - HYPOTHETICAL 46.7 KD PROTEIN IN CLB6- SPT6 INTERGENIC REGION | UNCLASSIFIED | 1003, 1006, 1008, 1038 |
| 7410 | 79951236 (13683, 13684) | Novel Protein sim. GBank g 1723722 sp P53299 YG3T_YEAST - HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631- KRE11 INTERGENIC REGION | UNCLASSIFIED | 1001 |
| 7411 | 57292347 (15071, 15072) | Novel Protein sim. GBank g 1723723 sp P53291 YG3U_YEAST - VERY HYPOTHETICAL 13.2 KD PROTEIN IN TIF4631- KRE11 INTERGENIC REGION | UNCLASSIFIED | 1004, 1006, 1022, 1024, 1026, 1034, 1038 |
| 7412 | 19883491 (4115, 4116) | Novel Protein sim. GBank g 1723744 sp P50078 YG4P_YEAST - HYPOTHETICAL 69.6 KD PROTEIN IN MRPL9- PET54 INTERGENIC REGION | UNCLASSIFIED | 1022 |
| 7413 | 79824860 (8845, 8846) | Novel Protein sim. GBank g 1723760 sp P53311 YG56_YEAST - HYPOTHETICAL 16.2 KD PROTEIN IN PFK1- TDS4 INTERGENIC REGION | UNCLASSIFIED | 1003, 1025, 1044 |
| 7414 | 27849068 (17725, 17726) | Novel Protein sim. GBank g 1723800 sp P25338 YGB0_YEAST - HYPOTHETICAL 20.2 KD PROTEIN IN PRS2- LEU1 INTERGENIC REGION | UNCLASSIFIED | 1022, 1034 |
| 7415 | 8489295 (11827, 11828) | Novel Protein sim. GBank g 1723843 sp P53168 YG51_YEAST - HYPOTHETICAL 27.5 KD PROTEIN IN PYC1- UBC2 INTERGENIC REGION | UNCLASSIFIED | 1024 |

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| 7416 | 79569167 (11441, 11442) | Novel Protein sim. GBank gil1723889 sp P40719 YGLY_ECOLI - PROBABLE SENSOR PROTEIN YGLY | | UNCLASSIFIED | 1006, 1017, 1022, 1054 |
| 7417 | 27955258 (13659, 13660) | Novel Protein sim. GBank gil172392 sp P53121 YGN9_YEAST - HYPOTHETICAL 90.8 KD PROTEIN IN MRF1-SEC27 INTERGENIC REGION | | UNCLASSIFIED | 1038 |
| 7418 | 10326965 (1325, 1326) | Novel Protein sim. GBank gil1723963 sp P53076 YGX7_YEAST - HYPOTHETICAL 108.2 KD PROTEIN IN SAP4-OST5 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1006, 1026, 1039 |
| 7419 | 80249073 (17413, 17414) | Novel Protein sim. GBank gil172403 sp P53633 YIPC_YEAST - YIP3 PROTEIN | | UNCLASSIFIED | 1044 |
| 7420 | 32122293 (243, 244) | Novel Protein sim. GBank gil1729735 emb CAA70933 - (Y09798) function unknown [Pseudomonas fluorescens] | | UNCLASSIFIED | 1024 |
| 7421 | 10920689 (21007, 21008) | Novel Protein sim. GBank gil1729852 sp Q02457 TBF1_YEAST - TBF1 PROTEIN (TTAGGG REPEAT-BINDING FACTOR 1) (TBF ALPHA) | | UNCLASSIFIED | 1006, 1009, 1023, 1025, 1034, 1044 |
| 7422 | 39564523 (1431, 1432) | Novel Protein sim. GBank gil1730572 sp P52960 PIP2_YEAST - PEROXISOME PROLIFERATION TRANSCRIPTIONAL REGULATOR | | UNCLASSIFIED | 1004, 1006, 1008, 1009, 1016, 1022, 1034, 1038, 1044 |
| 7423 | 80217521 (14595, 14596) | Novel Protein sim. GBank gil1723521 sp P52960 PIP2_YEAST - PEROXISOME PROLIFERATION TRANSCRIPTIONAL REGULATOR | | UNCLASSIFIED | 1006, 1010, 1022 |
| 7424 | 57292902 (1719, 1720) | Novel Protein sim. GBank gil1730592 sp P49954 YL85_YEAST - HYPOTHETICAL 32.6 KD PROTEIN YLR351C | | UNCLASSIFIED | 1001, 1017, 1025, 1038 |
| 7425 | 79865528 (2669, 2670) | Novel Protein sim. GBank gil1730621 sp P53759 YMI0_YEAST - HYPOTHETICAL 48.1 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION | | UNCLASSIFIED | |

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|------------------------|---|--|--------------|--|
| 7433 20008) | 79262053 (20007, Novel Protein sim. GBank gii1730729 sp P53951 YNE7_YEAST - HYPOTHETICAL 74.8 KD PROTEIN IN A1(G11. | | | |
| 7426 12350) | 94321703 (12349, Novel Protein sim. GBank gii1730634 sp P53845 YN03_YEAST - HYPOTHETICAL 35.5 KD PROTEIN IN PIK1- POL2 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1017, 1022, 1024, 1026, 1031, 1034, 1038, 1044 |
| 7427 13924) | 79254194 (13923, Novel Protein sim. GBank gii1730634 sp P53845 YN03_YEAST - HYPOTHETICAL 35.5 KD PROTEIN IN PIK1- POL2 INTERGENIC REGION | | UNCLASSIFIED | 1003 |
| 7428 9153, 9154) | 23290144 (9153, Novel Protein sim. GBank gii1730646 sp P53833 POP3_YEAST - RNA PROCESSING PROTEIN POP3 | | UNCLASSIFIED | 1017 |
| 7429 18784) | 78527204 (18783, Novel Protein sim. GBank gii1730665 sp P53721 YN89_YEAST - HYPOTHETICAL 25.3 KD PROTEIN IN TIM23- ARE2 INTERGENIC REGION | | UNCLASSIFIED | 1003 |
| 7430 3532) | 80277805 (3531, Novel Protein sim. GBank gii1730671 sp P53727 YN8F_YEAST - HYPOTHETICAL 35.4 KD PROTEIN IN SEC12- SSK2 INTERGENIC REGION | | UNCLASSIFIED | 1004, 1006, 1010, 1017, 1022, 1023, 1024, 1044 |
| 7431 5984) | 88093468 (5983, Novel Protein sim. GBank gii1730709 sp P53976 YNB8_YEAST - HYPOTHETICAL 69.6 KD PROTEIN IN HDA1- PUB1 INTERGENIC REGION | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1025, 1031, 1034, 1038, 1039, 1044, 1054 |
| 7432 16814) | 78747510 (16813, Novel Protein sim. GBank gii1730725 sp P53959 YNE1_YEAST - | | UNCLASSIFIED | 1026 |

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| 7442 | 8022641 (22751, 22752) | Novel Protein sim. GBank g 1731284 sp Q10815 YX25_MYCTU - PROBABLE INTEGRASE/RECOMBINASE CY274;25C | | UNCLASSIFIED | 1034 |
| 7443 | 17127322 (19371, 19372) | Novel Protein sim. GBank g 173164 (J02719) - valyl-tRNA synthetase [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1017 |
| 7444 | 66694404 (2407, 2408) | Novel Protein sim. GBank g 1732455 dbj BAA09692 - (D63377) 2-hydroxy-penta-2,4-denoate hydratase [Pseudomonas fluorescens] | | UNCLASSIFIED | 1009 |
| 7445 | 21637972 (2711, 2712) | Novel Protein sim. GBank g 1742118 dbj BAA14857 - (D90767) Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) [Escherichia coli] | | UNCLASSIFIED | 1039 |
| 7446 | 8501105 (4333, 4334) | Novel Protein sim. GBank g 1762939 (U66266) - ORF; able to induce HR-like lesions [Nicotiana tabacum] | | UNCLASSIFIED | 1004 |
| 7447 | 80061648 (21553, 21554) | Novel Protein sim. GBank g 177006 emb CA99555_1 - (Z75208) hypothetical protein [Bacillus subtilis] | | UNCLASSIFIED | 1024 |
| 7448 | 66694969 (10387, 10388) | Novel Protein sim. GBank g 1772622 (L39897) - HecB [Enterinia chrysanthemi] | | UNCLASSIFIED | 1009 |
| 7449 | 11102268 (21671, 21672) | Novel Protein sim. GBank g 1787014 (AE000181) - putative transcriptional regulator [Escherichia coli] | | UNCLASSIFIED | 1006 |
| 7450 | 10194321 (20201, 20202) | Novel Protein sim. GBank g 1787692 (AE000239) - orf, hypothetical protein [Escherichia coli] | | UNCLASSIFIED | 1003 |
| 7451 | 32164714 (22231, 22232) | Novel Protein sim. GBank g 1787799 (AE000249) - orf, hypothetical protein [Escherichia coli] | | UNCLASSIFIED | 1023 |
| 7452 | 78459813 (3273, 3274) | Novel Protein sim. GBank g 1788664 (AE000321) - putative peptidase [Escherichia coli] | | UNCLASSIFIED | 1026 |

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| 7453 | 27830844 (1489, 1490) | Novel Protein sim. GBank gil1788881 (AE000339) - putative ATP synthase beta subunit [Escherichia coli] | | UNCLASSIFIED | 1022 |
| 7454 | 16502457 (8883, 8884) | Novel Protein sim. GBank gil1794286 (U76606) - isobutylamine N-hydroxylase [Streptomyces viridifaciens] | | UNCLASSIFIED | 1008 |
| 7455 | 70949006 (22773, 22774) | Novel Protein sim. GBank gil1817699[emb CAB06573] - (Z84724) hypothetical protein Rv0433 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1029 |
| 7456 | 20622207 (17387, 17388) | Novel Protein sim. GBank gil1835414[emb CAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyerii] | | UNCLASSIFIED | 1004, 1025, 1034, 1039 |
| 7457 | 33198842 (13471, 13472) | Novel Protein sim. GBank gil1835124[emb CAA71005] - (Y09878) unnamed protein product [Mus musculus] | | UNCLASSIFIED | 1029 |
| 7458 | 79259307 (7561, 7562) | Novel Protein sim. GBank gil1835220[emb CAA62445] - (X90950) Rga1p (Dbm1p) [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1003, 1023 |
| 7459 | 54994425 (3679, 3680) | Novel Protein sim. GBank gil1838991[emb CAB06635] - (Z85982) lysX [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1029 |
| 7460 | 78453845 (7751, 7752) | Novel Protein sim. GBank gil1840087 (U83280) - 39 kDa antigen [Leishmania donovani] | | UNCLASSIFIED | 1026 |
| 7461 | 78374226 (12929, 12930) | Novel Protein sim. GBank gil1840087 (U83280) - 39 kDa antigen [Leishmania donovani] | | UNCLASSIFIED | 1003 |
| 7462 | 80421061 (12289, 12290) | Novel Protein sim. GBank gil1841968 (U67315) - unknown [Pseudomonas alcaligenes] | | UNCLASSIFIED | 1006, 1025 |
| 7463 | 18587497 (18539, 18540) | Novel Protein sim. GBank gil1850111[emb CAB06678] - (Z86059) hypothetical protein Rv0266c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1001 |
| 7464 | 28390204 (4475, 4476) | Novel Protein sim. GBank gil1864013[emb BAA13520] - (D87967) SHPS-1 (Mus musculus) | | UNCLASSIFIED | 1044 |

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| 7465 | 80244146 (14829, 14830) | Novel Protein sim. GBank gil1870003 emb CA06854 - (Z92539) hypothetical protein Rv1025 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1006, 1022, 1024 |
| 7466 | 20708208 (1609, 1610) | Novel Protein sim. GBank gil1870010 emb CA06861 - (Z92539) gilmU [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1006 |
| 7467 | 20473946 (8759, 8760) | Novel Protein sim. GBank gil1870011 emb CA06862 - (Z92539) psA [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1010 |
| 7468 | 30788874 (13143, 13144) | Novel Protein sim. GBank gil1877301 emb CA07144 - (Z92774) hypothetical protein Rv3570c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1016, 1026 |
| 7469 | 25263673 (11919, 11920) | Novel Protein sim. GBank gil1881254 dbj BAA19281 - (AB001488) SIMILAR TO C4-DICARBOXYLATE-BINDING PERIPLASMIC PROTEIN OF RHODOBACTER CAPSULATUS [Bacillus subtilis] | | UNCLASSIFIED | 1026 |
| 7470 | 94666728 (5995, 5996) | Novel Protein sim. GBank gil19006369 emb CAA72726 - (Y11998) hypothetical protein [Pseudomonas fluorescens] | | UNCLASSIFIED | 1006 |
| 7471 | 16499982 (17881, 17882) | Novel Protein sim. GBank gil1916229 (U83303) - line-1 reverse transcriptase [Homo sapiens] | | UNCLASSIFIED | 1030 |
| 7472 | 79488452 (19143, 19144) | Novel Protein sim. GBank gil1929089 emb CA07817 - (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1027 |
| 7473 | 78078007 (20613, 20614) | Novel Protein sim. GBank gil1934732 (U96128) - UDP-galactopyranose mutase [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1029 |
| 7474 | 36755672 (1729, 1730) | Novel Protein sim. GBank gil1938330 (U82303) - unknown [Homo sapiens] | | UNCLASSIFIED | 1034 |
| 7475 | 79831074 (20301, 20302) | Novel Protein sim. GBank gil1942485 pdb 1REQIB - Chain B, Methylmalonyl-Coa Mutase | | UNCLASSIFIED | 1023 |

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| 7476 | 81932612 (12826) 12826) | Novel Protein sim. GBank gi 1944391 dbj BAA193685 - (D86413) Ern4p [Saccharomyces cerevisiae] | UNCLASSIFIED | 1000, 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1026, 1027, 1031, 1034, 1038, 1039, 1044, 1054 |
| 7477 | 65667188 (4513, 4514) | Novel Protein sim. GBank gi 198646 (M29324) - ORF2; 5' end undetermined. [Mus musculus] | UNCLASSIFIED | 1054 |
| 7478 | 11084375 (6427, 6428) | Novel Protein sim. GBank gi 2058299 emb CAA66983 - (X98309) ARI protein [Drosophila melanogaster] | UNCLASSIFIED | 1010 |
| 7479 | 57292546 (2089), 20892) | Novel Protein sim. GBank gi 2062680 (U88964) - HEM45 [Homo sapiens] | UNCLASSIFIED | 1004, 1016 |
| 7480 | 78503017 (19097, 19098) | Novel Protein sim. GBank gi 2065209 emb CAA73250 - (Y12713) Gag polyprotein [Mus musculus] | UNCLASSIFIED | 1026 |
| 7481 | 71122286 (10953, 10954) | Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus] | UNCLASSIFIED | 1016 |
| 7482 | 80104933 (11695, 11696) | Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus] | UNCLASSIFIED | 1010 |
| 7483 | 65641894 (12781, 12782) | Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus] | UNCLASSIFIED | 1016 |
| 7484 | 79558374 (17197, 17198) | Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus] | UNCLASSIFIED | 1038 |
| 7485 | 46887745 (22711, 22712) | Novel Protein sim. GBank gi 2065210 emb CAA73251 - (Y12713) Pro-Pol- dUTPase polyprotein [Mus musculus] | UNCLASSIFIED | 1037 |

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| 7486 | 36732609 (13277, 13278) | Novel Protein sim. GBank gij2072948 (U93563) - putative p150 [Homo sapiens] | | UNCLASSIFIED | 1023 |
| 7487 | 866886154 (12379, 12380) | Novel Protein sim. GBank gij2072951 (U93564) - putative p150 [Homo sapiens] | | UNCLASSIFIED | 1018 |
| 7488 | 658886038 (17937, 17938) | Novel Protein sim. GBank gij2072951 (U93564) - putative p150 [Homo sapiens] | | UNCLASSIFIED | 1029 |
| 7489 | 65645483 (17415, 17416) | Novel Protein sim. GBank gij2072955 (U93566) - p40 [Homo sapiens] | | UNCLASSIFIED | 1041 |
| 7490 | 37014367 (1127, 1128) | Novel Protein sim. GBank gij2072967 (U93570) - putative p150 [Homo sapiens] | | UNCLASSIFIED | 1029 |
| 7491 | 78677077 (2303, 2304) | Novel Protein sim. GBank gij2072967 (U93570) - putative p150 [Homo sapiens] | | UNCLASSIFIED | 1026 |
| 7492 | 13523238 (16401, 16402) | Novel Protein sim. GBank gij2072967 (U93570) - putative p150 [Homo sapiens] | | UNCLASSIFIED | 1004 |
| 7493 | 30176122 (20253, 20254) | Novel Protein sim. GBank gij2072972 (U93572) - putative p150 [Homo sapiens] | | UNCLASSIFIED | 1029 |
| 7494 | 19882024 (1599, 1600) | Novel Protein sim. GBank gij2076670[emb CAB08387] - (Z95150) hypothetical protein Rv3095 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1034 |
| 7495 | 85806873 (18477, 18478) | Novel Protein sim. GBank gij2078009[emb CAB08456] - (Z95207) hypothetical protein Rv2850c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1054 |
| 7496 | 95287796 (14669, 14670) | Novel Protein sim. GBank gij2078024[emb CAB08477] - (Z95208) hypothetical protein Rv2375 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1006, 1008, 1009, 1012, 1024 |
| 7497 | 80478399 (3825, 3826) | Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycopeptide AFGP polyprotein precursor Boreogadus saida] | | UNCLASSIFIED | 1012 |
| 7498 | 80048270 (16845, 16846) | Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycopeptide AFGP polyprotein precursor Boreogadus saida] | | UNCLASSIFIED | 1004, 1027 |
| 7499 | 80469619 (20951, 20952) | Novel Protein sim. GBank gij2094844[emb CAB08571] - (Z95324) fba [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012, 1038 |

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| 7500 | 19880484 (14413, 14414) | Novel Protein sim. GBank gij 2104338 emb CAB08653 - (Z95388) Hypothetical protein Rv2140c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1034 |
| 7501 | 37801575 (5187, 5188) | Novel Protein sim. GBank gij 2104375 emb CAB08718 - (Z95390) Hypothetical protein Rv3452 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012 |
| 7502 | 78240045 (5217, 5218) | Novel Protein sim. GBank gij 2104600 emb CAB08809 - (Z95398) unknown [Mycobacterium leprae] | | UNCLASSIFIED | 1026 |
| 7503 | 35062334 (18629, 18630) | Novel Protein sim. GBank gij 2113990 emb CAB08995 - (Z95558) Hypothetical protein Rv0528 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1024 |
| 7504 | 78481280 (18653, 18654) | Novel Protein sim. GBank gij 2114473 (U96963) - p 40mDia [Mus musculus] | | UNCLASSIFIED | 1026 |
| 7505 | 65680609 (2035, 2036) | Novel Protein sim. GBank gij 2117310 emb CAB09116.1 - (Z95620) Hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1030, 1041 |
| 7506 | 46571634 (7333, 7334) | Novel Protein sim. GBank gij 2117310 emb CAB09116.1 - (Z95620) Hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1029 |
| 7507 | 78905075 (8509, 8510) | Novel Protein sim. GBank gij 2117310 emb CAB09116.1 - (Z95620) Hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1003 |
| 7508 | 78300286 (2877, 2878) | Novel Protein sim. GBank gij 2119898 pir S49550 - IM-like protein emmL9 - Streptococcus pyogenes (strain 71-683) | | UNCLASSIFIED | 1030, 1054 |
| 7509 | 80040488 (19007, 19008) | Novel Protein sim. GBank gij 2120070 pir S69973 - TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty2.N | | UNCLASSIFIED | 1004, 1006, 1058 |

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| 7521 | 57530381 (5625, 5626) | Novel Protein sim. GBank gi 2131367 pir S67786 hypothetical protein YDL223c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1006, 1012, 1017, 1022, 1024, 1026, 1034 |
| 7522 | 65481450 (59, 60) | Novel Protein sim. GBank gi 2131404 pir S70126 - hypothetical protein YDR266c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1049 |
| 7523 | 80044676 (12949, 12950) | Novel Protein sim. GBank gi 2131443 pir S61155 - hypothetical protein YDR359c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006 |
| 7524 | 29449628 (45, 46) | Novel Protein sim. GBank gi 2131446 pir S61157 - hypothetical protein YDR362c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1026 |
| 7525 | 78747500 (14261, 14262) | Novel Protein sim. GBank gi 2131449 pir S69746 - hypothetical protein YDR366c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1026 |
| 7526 | 80205726 (9709, 9710) | Novel Protein sim. GBank gi 2131466 pir S69681 - hypothetical protein YDR398w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006, 1008, 1017, 1022, 1024, 1025, 1026, 1034, 1038 |
| 7527 | 27835905 (7661, 7662) | Novel Protein sim. GBank gi 2131501 pir S69731 - hypothetical protein YDR452w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1006, 1024, 1034 |
| 7528 | 27838166 (4411, 4412) | Novel Protein sim. GBank gi 2131505 pir S69625 - hypothetical protein YDR457w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1024 |
| 7529 | 8359866 (15541, 15542) | Novel Protein sim. GBank gi 2131510 pir S69634 - hypothetical protein YDR466w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1024 |
| 7530 | 27963931 (10999, 11000) | Novel Protein sim. GBank gi 2131529 pir S69680 - hypothetical protein YDR493w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1006, 1034 |

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| 7531 | 80431196 (6761, 6762) | Novel Protein sim. GBank gi 2131541 pir S69574 - hypothetical protein YDR517w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1001, 1003, 1006, 1008, 1012, 1016, 1017, 1022, 1023, 1024, 1026, 1031, 1034, 1038, 1039, 1044 |
| 7532 | 80502906 (4781, 4782) | Novel Protein sim. GBank gi 2131542 pir S69577 - hypothetical protein YDR520c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1006, 1010, 1012, 1017, 1022, 1024, 1034 |
| 7533 | 80478058 (17271, 17272) | Novel Protein sim. GBank gi 2131542 pir S69577 - hypothetical protein YDR520c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1006, 1008, 1009, 1012, 1022, 1023, 1024, 1026, 1030, 1034, 1039 |
| 7534 | 80019606 (9793, 9794) | Novel Protein sim. GBank gi 2131545 pir S69581 - hypothetical protein YDR525w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006, 1025, 1027, 1034 |
| 7535 | 79625779 (441, 442) | Novel Protein sim. GBank gi 2131548 pir S69583 - hypothetical protein YDR528w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006, 1017 |
| 7536 | 27842289 (3801, 3802) | Novel Protein sim. GBank gi 2131776 pir S64933 - hypothetical protein YLR099c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 7537 | 13519757 (2235, 2236) | Novel Protein sim. GBank gi 2131778 pir S64944 - hypothetical protein YLR107w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1024 |
| 7538 | 95011183 (21845, 21846) | Novel Protein sim. GBank gi 2131791 pir S65003 - hypothetical protein YLR154c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1001, 1003, 1004, 1010, 1012, 1022, 1023, 1024, 1026 |

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| 7539 10370) | 57294978 (10369, Novel Protein sim. GBank gi 2131820 pir S69871 - hypothetical protein YML012c-a - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1006, 1008, 1022, 1024, 1031, 1034, 1038 |
| 7540 80226467 (6279, 6280) | Novel Protein sim. GBank gi 2131887 pir S66717 - hypothetical protein YOL034w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1008, 1009, 1017, 1022, 1024, 1026, 1034, 1039 |
| 7541 79318993 (2487, 2468) | Novel Protein sim. GBank gi 2132008 pir S66765 - hypothetical protein YOL072w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1034 |
| 7542 78677090 (5093, 5094) | Novel Protein sim. GBank gi 2132036 pir S66923 - hypothetical protein YOR049c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1026 |
| 7543 3696917 (12291, 12292) | Novel Protein sim. GBank gi 2132046 pir S66953 - hypothetical protein YOR070c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1012 |
| 7544 30404307 (19565, 19566) | Novel Protein sim. GBank gi 2132048 pir S66959 - hypothetical protein YOR076c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1008 |
| 7545 30404479 (20045, 20046) | Novel Protein sim. GBank gi 2132048 pir S66959 - hypothetical protein YOR076c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1008 |
| 7546 85513670 (4671, 4672) | Novel Protein sim. GBank gi 2132051 pir S61644 - hypothetical protein YOR083w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1001, 1003, 1006, 1010, 1017, 1022, 1023, 1034, 1039, 1044, 1049 |
| 7547 80240865 (8373, 8374) | Novel Protein sim. GBank gi 2132058 pir S61668 - hypothetical protein YOR110w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1016, 1017, 1022, 1023, 1024, 1026, 1034, 1039, 1044, 1054 |

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| 7548 | 78742231 (11281, 11282) | Novel Protein sim. GBank gi 2132066 pir S60988 - hypothetical protein YOR134w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1022 |
| 7549 | 17743829 (13223, 13224) | Novel Protein sim. GBank gi 2132067 pir S61698 - hypothetical protein YOR144c - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1044 |
| 7550 | 27844553 (5643, 5644) | Novel Protein sim. GBank gi 2132087 pir S60947 - hypothetical protein YOR220w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1006 |
| 7551 | 30256586 (11755, 11756) | Novel Protein sim. GBank gi 2132103 pir S67155 - hypothetical protein YOR258w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1024 |
| 7552 | 80216691 (19881, 19882) | Novel Protein sim. GBank gi 2132113 pir S67186 - hypothetical protein YOR284w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1003, 1004, 1006, 1008, 1009, 1010, 1022, 1024, 1026, 1027, 1030, 1034, 1038, 1039, 1044 |
| 7553 | 80428123 (7417, 7418) | Novel Protein sim. GBank gi 2132147 pir S59679 - hypothetical protein YPL014w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1003, 1004, 1006, 1024, 1025, 1034 |
| 7554 | 20262048 (21789, 21790) | Novel Protein sim. GBank gi 2132153 pir S63458 - hypothetical protein YPL024w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1022 |
| 7555 | 5469539 (10377, 10378) | Novel Protein sim. GBank gi 2132186 pir S61970 - hypothetical protein YPL096w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1058 |
| 7556 | 86380059 (9757, 9758) | Novel Protein sim. GBank gi 2132189 pir S61960 - hypothetical protein YPL107w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1053 |
| 7557 | 65481779 (3725, 3726) | Novel Protein sim. GBank gi 2132190 pir S61959 - hypothetical protein YPL108w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1049 |
| 7558 | 78742085 (18459, 18460) | Novel Protein sim. GBank gi 2132232 pir S65227 - hypothetical protein YPL208w - yeast (<i>Saccharomyces cerevisiae</i>) | | UNCLASSIFIED | 1008, 1009, 1022, 1039 |

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| 7559 | 79111339 (12103, 12104) | Novel Protein sim. GBank g 2132241 pir S61701 hypothetical protein YPL233w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1039 |
| 7560 | 79579586 (2157, 2158) | Novel Protein sim. GBank g 2132244 pir S61023 hypothetical protein YPL242c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1004, 1022 |
| 7561 | 80219478 (6659, 6660) | Novel Protein sim. GBank g 2132265 pir S70044 hypothetical protein YPR077c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1004, 1029, 1034, 1039 |
| 7562 | 80479572 (19531, 19532) | Novel Protein sim. GBank g 2132273 pir S69074 hypothetical protein YPR090w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1009, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1026, 1027, 1034, 1039, 1044 |
| 7563 | 52557997 (21467, 21468) | Novel Protein sim. GBank g 2132273 pir S69074 hypothetical protein YPR090w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1054 |
| 7564 | 80219161 (13661, 13662) | Novel Protein sim. GBank g 2132285 pir S59773 hypothetical protein YPR108w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1004, 1006, 1010, 1017, 1022, 1023, 1025, 1031 |
| 7565 | 80227275 (1597, 1598) | Novel Protein sim. GBank g 2132299 pir S69029 hypothetical protein YPR140w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1022, 1034 |
| 7566 | 10251496 (10445, 10446) | Novel Protein sim. GBank g 2132313 pir S59830 hypothetical protein YPR172w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1038 |
| 7567 | 79256284 (2865, 2866) | Novel Protein sim. GBank g 2132353 pir S42160 MSS51 protein - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1003, 1022 |

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| 7568 29680966 (19215, 19216) | Novel Protein sim. GBank g 2132444 pir S67694 - probable membrane protein YDL146w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1009 |
| 7569 27824338 (13079, 13080) | Novel Protein sim. GBank g 2132460 pir S67781 - probable membrane protein YDL218w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1024 |
| 7570 11304673 (22139, 22140) | Novel Protein sim. GBank g 2132462 pir S67794 - probable membrane protein YDL231c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1034 |
| 7571 78791459 (4743, 4744) | Novel Protein sim. GBank g 2132487 pir S70134 - probable membrane protein YDR278c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 7572 28397253 (11401, 11402) | Novel Protein sim. GBank g 2132491 pir S70114 - probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1039 |
| 7573 94672659 (1619, 1620) | Novel Protein sim. GBank g 2132502 pir S59792 - probable membrane protein YDR326c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 7574 95295893 (6197, 6198) | Novel Protein sim. GBank g 2132508 pir S61149 - probable membrane protein YDR352w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022, 1025 |
| 7575 80205918 (2025, 2026) | Novel Protein sim. GBank g 2132649 pir S64771 - probable membrane protein YLL023c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1008, 1022, 1024, 1025, 1026, 1034, 1038 |
| 7576 80216897 (21771, 21772) | Novel Protein sim. GBank g 2132649 pir S64771 - probable membrane protein YLL023c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003, 1006, 1008, 1022, 1024, 1034, 1039, 1044 |

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| 7577 | 37010090 (6351, 6352) | Novel Protein sim. GBank gi 2132661 pir S64842 - probable membrane protein YLR020c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1029 |
| 7578 | 94239989 (21231, 21232) | Novel Protein sim. GBank gi 2132663 pir S64851 - probable membrane protein YLR024c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1017 |
| 7579 | 28471139 (17711, 17712) | Novel Protein sim. GBank gi 2132667 pir S64869 - probable membrane protein YLR042c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1008 |
| 7580 | 80215889 (10567, 10568) | Novel Protein sim. GBank gi 2132679 pir S64916 - probable membrane protein YLR084c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1006, 1010, 1022, 1024, 1034 |
| 7581 | 30645909 (11855, 11856) | Novel Protein sim. GBank gi 2132679 pir S64916 - probable membrane protein YLR084c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1008 |
| 7582 | 27838227 (17267, 17268) | Novel Protein sim. GBank gi 2132680 pir S64921 - probable membrane protein YLR087c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006 |
| 7583 | 23288283 (4893, 4894) | Novel Protein sim. GBank gi 2132817 pir S61981 - probable membrane protein YOL003c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003 |
| 7584 | 11594169 (18327, 18328) | Novel Protein sim. GBank gi 2132839 pir S66766 - probable membrane protein YOL073c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1034 |
| 7585 | 78385738 (13647, 13648) | Novel Protein sim. GBank gi 2132846 pir S66816 - probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1026 |

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| 7586 | 82056110 (10809, 10810) | Novel Protein sim. GBank gi 2 32852 pir S66835 - probable membrane protein YOL138c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006, 1010, 1016, 1022, 1024 |
| 7587 | 79861380 (15847, 15848) | Novel Protein sim. GBank gi 2 32852 pir S66835 - probable membrane protein YOL138c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1025 |
| 7588 | 80216050 (14435, 14436) | Novel Protein sim. GBank gi 2 32853 pir S60390 - probable membrane protein YOL146w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006, 1024, 1025, 1026, 1039 |
| 7589 | 95295784 (8587, 8588) | Novel Protein sim. GBank gi 2 32878 pir S61645 - probable membrane protein YOR084w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1001, 1006, 1008, 1017, 1022, 1023, 1038 |
| 7590 | 27974805 (15461, 15462) | Novel Protein sim. GBank gi 2 32880 pir S66972 - probable membrane protein YOR087w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006 |
| 7591 | 8371339 (10795, 10796) | Novel Protein sim. GBank gi 2 32882 pir S61654 - probable membrane protein YOR093c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1004 |
| 7592 | 94655445 (4283, 4284) | Novel Protein sim. GBank gi 2 32889 pir S61667 - probable membrane protein YOR109w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1001, 1003, 1004, 1006, 1008, 1010, 1012, 1016, 1017, 1022, 1023, 1024, 1034, 1038, 1039 |
| 7593 | 80217723 (17475, 17476) | Novel Protein sim. GBank gi 2 32900 pir S67042 - probable membrane protein YOR154w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006, 1008, 1022, 1024 |

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| 7594 6766) | 20687093 (6765, probable membrane protein YOR161c - yeast (Saccharomyces cerevisiae) | Novel Protein sim. GBank gi 2132901 pir S67049 probable membrane protein YOR161c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1024 |
| 7595 80232671 (10687, 10688) | Novel Protein sim. GBank gi 2132902 pir S67050 probable membrane protein YOR162c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1004, 1008, 1009, 1022, 1044 |
| 7596 29346134 (9567, 9568) | Novel Protein sim. GBank gi 2132903 pir S67053 probable membrane protein YOR165w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1022 |
| 7597 11302078 (18577, 18578) | Novel Protein sim. GBank gi 2132903 pir S67053 probable membrane protein YOR165w - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1024 |
| 7598 20728259 (1975, 1976) | Novel Protein sim. GBank gi 2132917 pir S60941 probable membrane protein YOR214c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006 |
| 7599 39547842 (2179, 2180) | Novel Protein sim. GBank gi 2132942 pir S67210 probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1006, 1010, 1022, 1024, 1031, 1034 |
| 7600 78891211 (5569, 5570) | Novel Protein sim. GBank gi 2132947 pir S58333 probable membrane protein YOR322c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1003 |
| 7601 78780706 (11765, 11766) | Novel Protein sim. GBank gi 2132947 pir S58333 probable membrane protein YOR322c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1009 |
| 7602 17882403 (22047, 22048) | Novel Protein sim. GBank gi 2132947 pir S58333 probable membrane protein YOR322c - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1039 |

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| 7603 | 80216496 (21086) 21086) | Novel Protein sim. GBank gi 2132965 pir S67303 - probable membrane protein YOR391c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1004, 1006, 1008, 1010, 1017, 1022, 1024, 1031, 1034, 1038 |
| 7604 | 37810436 (1649, 1650) | Novel Protein sim. GBank gi 2132974 pir S60930 - probable membrane protein YPL060w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1058 |
| 7605 | 30643448 (13617, 13618) | Novel Protein sim. GBank gi 2132975 pir S61116 - probable membrane protein YPL070w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1022 |
| 7606 | 80221176 (11241, 11242) | Novel Protein sim. GBank gi 2132983 pir S62009 - probable membrane protein YPL112c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1006, 1008, 1009, 1010, 1017, 1022, 1024, 1025 |
| 7607 | 17088016 (20927, 20928) | Novel Protein sim. GBank gi 2133004 pir S65240 - probable membrane protein YPL221w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1023 |
| 7608 | 65466546 (22787, 22788) | Novel Protein sim. GBank gi 2133004 pir S65240 - probable membrane protein YPL221w - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1010 |
| 7609 | 80227049 (22957, 22958) | Novel Protein sim. GBank gi 2133006 pir S61026 - probable membrane protein YPL238c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1004, 1006, 1008, 1017, 1024, 1034 |
| 7610 | 78516982 (16291, 16292) | Novel Protein sim. GBank gi 2133016 pir S65310 - probable membrane protein YPL277c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1008 |
| 7611 | 26241287 (17817, 17818) | Novel Protein sim. GBank gi 2133023 pir S69075 - probable membrane protein YPR091c - yeast (Saccharomyces cerevisiae) | UNCLASSIFIED | 1009 |

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| 7612 | 16389007 (5307, 5308) | Novel Protein sim. GBank g 2133025 pir S59770 - probable membrane protein YPR105c - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1017 |
| 7613 | 98802917 (4357, 4358) | Novel Protein sim. GBank g 2133031 pir S69028 - probable membrane protein YPR139c - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1001, 1004, 1006, 1010, 1012, 1022, 1023, 1025, 1054 |
| 7614 | 79818070 (11643, 11644) | Novel Protein sim. GBank g 2133039 pir S59841 - probable membrane protein YPR184w - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1006 |
| 7615 | 28471403 (15925, 15926) | Novel Protein sim. GBank g 2133039 pir S59841 - probable membrane protein YPR184w - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1026 |
| 7616 | 78769950 (18637, 18638) | Novel Protein sim. GBank g 2133082 pir S67314 - regulatory protein MSR1 - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1026 |
| 7617 | 27803028 (21833, 21834) | Novel Protein sim. GBank g 2133082 pir S67314 - regulatory protein MSR1 - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1003, 1004, 1024, 1034 |
| 7618 | 20726205 (8205, 8206) | Novel Protein sim. GBank g 2133091 pir S61716 - ribose-phosphate pyrophosphokinase PRPS3 homolog YOL061w - yeast (<i>Saccharomyces cerevisiae</i>) | UNCLASSIFIED | 1006 |
| 7619 | 10170101 (13213, 13214) | Novel Protein sim. GBank g 2137043 pir I46880 - unknown protein - rabbit (fragment) | UNCLASSIFIED | 1025 |
| 7620 | 94126265 (297, 298) | Novel Protein sim. GBank g 2137756 pir I48746 - semaphorin C - mouse (fragment) | UNCLASSIFIED | 1053 |
| 7621 | 35108236 (22163, 22164) | Novel Protein sim. GBank g 2143878 pir I55615 - nitric-oxide synthase (EC 1.14.13.39) - rat | UNCLASSIFIED | 1050 |

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| 7622 | 78763064 (17237, 17238) | Novel Protein sim. GBank gj 2144206 p1r S63664 - hypothetical protein 211 - Allomyces macrogyrus mitochondrial | | UNCLASSIFIED | 1008, 1039 |
| 7623 | 11102552 (5743, 5744) | Novel Protein sim. GBank gj 2145653 p1r S72762 - B1496_C2_194 protein - Mycobacterium leprae | | UNCLASSIFIED | 1006 |
| 7624 | 78785069 (537, 538) | Novel Protein sim. GBank gj 2146836 p1r S74280 - hypothetical protein YCL054W - yeast (Saccharomyces cerevisiae) | | UNCLASSIFIED | 1008, 1009, 1022 |
| 7625 | 27381118 (15161, 15162) | Novel Protein sim. GBank gj 215574 (M64097) - E16 [Bacteriophage mu] | | UNCLASSIFIED | 1006 |
| 7626 | 79480752 (3833, 3834) | Novel Protein sim. GBank gj 2183285 (AF002860) - tuftelin [Mus musculus] | | UNCLASSIFIED | 1022, 1055 |
| 7627 | 79367999 (1171, 1172) | Novel Protein sim. GBank gj 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus] | | UNCLASSIFIED | 1034 |
| 7628 | 87465696 (8893, 8894) | Novel Protein sim. GBank gj 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus] | | UNCLASSIFIED | 1018 |
| 7629 | 65445062 (22553, 22554) | Novel Protein sim. GBank gj 2193870 dbj BAA20419 - (D84391) reverse transcriptase [Mus musculus] | | UNCLASSIFIED | 1038 |
| 7630 | 78047124 (22063, 22064) | Novel Protein sim. GBank gj 2196970 (U83169) - polythreonine protein [Cryptosporidium parvum] | | UNCLASSIFIED | 1054 |
| 7631 | 29020343 (19237, 19238) | Novel Protein sim. GBank gj 2213429 emb CAA63344 - (X92653) unknown product [Drosophila melanogaster] | | UNCLASSIFIED | 1017 |
| 7632 | 79425557 (4181, 4182) | Novel Protein sim. GBank gj 2224685 dbj BAA20827 - (AB002370) KIAA0372 [Homo sapiens] | | UNCLASSIFIED | 1038 |
| 7633 | 46571958 (15143, 15144) | Novel Protein sim. GBank gj 2224829 emb CAB10017 - (Z97188) hypothetical protein Rv3816c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1029 |

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| 7634 | 8176133 (3977, 3978) | Novel Protein sim. GBank gil2224832 emb[CAB10018] - (Z97188) hypothetical protein Rv3813c [Mycobacterium tuberculosis] | UNCLASSIFIED | |
| 7635 | 78980140 (3431, 3432) | Novel Protein sim. GBank gil2226004 (U49973) - ORF1; MER37; putative transposase similar to pogo element [Homo sapiens] | UNCLASSIFIED | 1008 |
| 7636 | 65506326 (8355, 8356) | Novel Protein sim. GBank gil2226004 (U49973) - ORF1; MER37; putative transposase similar to pogo element [Homo sapiens] | UNCLASSIFIED | 1016 |
| 7637 | 78717291 (13389, 13390) | Novel Protein sim. GBank gil2226004 (U49973) - ORF1; MER37; putative transposase similar to pogo element [Homo sapiens] | UNCLASSIFIED | 1025 |
| 7638 | 30393743 (18127, 18128) | Novel Protein sim. GBank gil2226004 (U49973) - ORF1; MER37; putative transposase similar to pogo element [Homo sapiens] | UNCLASSIFIED | 1054 |
| 7639 | 33189257 (6993, 6994) | Novel Protein sim. GBank gil2226005 (U49973) - ORF2; function unknown [Homo sapiens] | UNCLASSIFIED | 1026 |
| 7640 | 55489578 (16875, 16876) | Novel Protein sim. GBank gil2226005 (U49973) - ORF2; function unknown [Homo sapiens] | UNCLASSIFIED | 1026 |
| 7641 | 94641276 (2965, 2966) | Novel Protein sim. GBank gil2239236 emb[CAB10154] - (Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe] | UNCLASSIFIED | 1034 |
| 7642 | 7542334 (7253, 7254) | Novel Protein sim. GBank gil2244807 emb[CAB10230.1] - (Z97336) hypothetical protein [Arabidopsis thaliana] | UNCLASSIFIED | 1058 |
| 7643 | 30161837 (3019, 3020) | Novel Protein sim. GBank gil2244854 emb[CAB10276.1] - (Z97337) hypothetical [Arabidopsis thaliana] | UNCLASSIFIED | 1016 |
| 7644 | 11291903 (14785, 14786) | Novel Protein sim. GBank gil2252812 gb AAB62820.1 - (AF004731) Stp22p [Saccharomyces cerevisiae] | UNCLASSIFIED | 1024 |
| 7645 | 78740549 (7517, 7518) | Novel Protein sim. GBank gil2253535 gb AAB63256.1 - (J69172) unknown [Mus musculus] | UNCLASSIFIED | 1039 |

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| 7646 | 79574930 (9543, 9544) | Novel Protein sim. GBank gil22577/08 (U73041) - transposase-like protein [Thiobacillus ferrooxidans] | | UNCLASSIFIED | 1031 |
| 7647 | 10141524 (3623, 3624) | Novel Protein sim. GBank gil2271391 (AF009352) - osmoprotectant binding protein precursor [Bacillus subtilis] | | UNCLASSIFIED | 1025 |
| 7648 | 79552136 (8551, 8552) | Novel Protein sim. GBank gil2276407 (L77975) - homospermidine synthase [Blastochloris viridis] | | UNCLASSIFIED | 1039 |
| 7649 | 13763445 (2925, 2926) | Novel Protein sim. GBank gil2280480[gb]BA21572] - (AB002344) KIAA0346 [Homo sapiens] | | UNCLASSIFIED | 1016 |
| 7650 | 86473972 (19637, 19638) | Novel Protein sim. GBank gil2291142 (AF016417) - No definition line found [Caenorhabditis elegans] | | UNCLASSIFIED | 1054 |
| 7651 | 11291481 (17135, 17136) | Novel Protein sim. GBank gil2292957[emb]CAB10899] - (Z98209) hypothetical protein Rv2723 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1010 |
| 7652 | 30371494 (18453, 18454) | Novel Protein sim. GBank gil2292986[emb]CAA04133] - (AJ000496) cyclic nucleotide-gated channel beta subunit [Rattus norvegicus] | | UNCLASSIFIED | 1016 |
| 7653 | 20622189 (15233, 15234) | Novel Protein sim. GBank gil2293257 (AF008220) - YtnM [Bacillus subtilis] | | UNCLASSIFIED | 1004 |
| 7654 | 14206236 (9761, 9762) | Novel Protein sim. GBank gil2313487[gb]ADD07451.1] - (AE000555) zinc-metallo protease [YJR117W] [Helicobacter pylori 26695] | | UNCLASSIFIED | 1053 |
| 7655 | 14219143 (19543, 19544) | Novel Protein sim. GBank gil2313638[gb]ADD07591.1] - (AE000566) cag pathogenicity island protein (cag5) [Helicobacter pylori 26695] | | UNCLASSIFIED | 1034 |
| 7656 | 14207029 (20955, 20956) | Novel Protein sim. GBank gil2313798[gb]ADD07737.1] - (AE000580) H. pylori predicted coding region HP0669 [Helicobacter pylori 26695] | | UNCLASSIFIED | 1034 |

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| 7657 | 20267403 (19431, 19432), | Novel Protein sim. GBank gi 2313817 gb AAD07745.1 - (AE000582) conserved hypothetical integral membrane protein [Helicobacter pylori 26695] | UNCLASSIFIED | 1010 |
| 7658 | 13883812 (12061, 12062) | Novel Protein sim. GBank gi 2313940 gb AAD07858.1 - (AE000592) H. pylori predicted coding region HP0803 [Helicobacter pylori 26695] | UNCLASSIFIED | 1053 |
| 7659 | 39523975 (15849, 15850) | Novel Protein sim. GBank gi 2313984 gb AAD07898.1 - (AE000596) type I restriction enzyme M protein (rsdM) [Helicobacter pylori 26695] | UNCLASSIFIED | 1004 |
| 7660 | 80209487 (10329, 10330) | Novel Protein sim. GBank gi 2314013 gb AAD07926.1 - (AE000597) H. pylori predicted coding region HP0874 [Helicobacter pylori 26695] | UNCLASSIFIED | 1034 |
| 7661 | 80209530 (20299, 20300) | Novel Protein sim. GBank gi 2314144 gb AAD08046.1 - (AE000608) H. pylori predicted coding region HP0996 [Helicobacter pylori 26695] | UNCLASSIFIED | 1034 |
| 7662 | 57288608 (4083, 4084) | Novel Protein sim. GBank gi 2314247 gb AAD08141.1 - (AE000616) conserved hypothetical secreted protein [Helicobacter pylori 26695] | UNCLASSIFIED | 1053 |
| 7663 | 20287152 (17523, 17524) | Novel Protein sim. GBank gi 2314381 gb AAD08264.1 - (AE000627) D- lactate dehydrogenase (ldh) [Helicobacter pylori 26695] | UNCLASSIFIED | 1034 |
| 7664 | 13886351 (5621, 5622) | Novel Protein sim. GBank gi 2314680 gb AAD08542.1 - (AE000648) glutamate permease (gltS) [Helicobacter pylori 26695] | UNCLASSIFIED | 1053 |
| 7665 | 20603459 (8711, 8712) | Novel Protein sim. GBank gi 2326734 emb CAB10948 - (Z98288) hypothetical protein Rv1691 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1004 |

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| 7666 | 77474079 (287, 288) | Novel Protein sim. GBank gi 2340009 emb CAB11359 - (Z98682) Y1bm protein [Bacillus subtilis] | | UNCLASSIFIED | 1023, 1026 |
| 7667 | 24129321 (21639, 21640) | Novel Protein sim. GBank gi 2340850 emb CAA74067 - (Y13732) urease accessory protein [Ralstonia eutropha] | | UNCLASSIFIED | 1003 |
| 7668 | 655708325 (7393, 7394) | Novel Protein sim. GBank gi 2341020 gb AAC35295 - (AC002483) putative product from mRNA sequence CG003 from BRCA2 region; match to U50534 (NID:91685103) [Homo sapiens] | | UNCLASSIFIED | 1001, 1038 |
| 7669 | 25233410 (11813, 11814) | Novel Protein sim. GBank gi 2341020 gb AAC35295 - (AC002483) putative product from mRNA sequence CG003 from BRCA2 region; match to U50534 (NID:91685103) [Homo sapiens] | | UNCLASSIFIED | 1017 |
| 7670 | 28359669 (18123, 18124) | Novel Protein sim. GBank gi 2342526 emb CAA74694 - (Y14314) IgE autoantigen [Homo sapiens] | | UNCLASSIFIED | 1025 |
| 7671 | 47652669 (25, 26) | Novel Protein sim. GBank gi 2344830 emb CAA94727 - (Z70722) leucy- l tRNA synthetase [Mycobacterium leprae] | | UNCLASSIFIED | 1029 |
| 7672 | 91254054 (15457, 15458) | Novel Protein sim. GBank gi 2369714 emb CAB09900 - (Z97178) elongation factor 2 [Beta vulgaris] | | UNCLASSIFIED | 1010 |
| 7673 | 11234033 (2077, 2078) | Novel Protein sim. GBank gi 2370478 emb CAB11506 - (Z98849) putative DNA repair helicase [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1022 |
| 7674 | 78890197 (13797, 13798) | Novel Protein sim. GBank gi 2384711 (AF013969) - antigen containing epitope to monoclonal antibody MMS-85/12 [Mus musculus] | | UNCLASSIFIED | 1003, 1008, 1017, 1044 |
| 7675 | 58253443 (13457, 13458) | Novel Protein sim. GBank gi 2384732 (AF015911) - NAC-1 protein [Rattus norvegicus] | | UNCLASSIFIED | 1058 |

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| 7676 | 11686492 (19935, 19936) | Novel Protein sim. GBank gi 2388986 emb CAB11718 - (Z98980) actin associated protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1004, 1031 |
| 7677 | 23333247 (5949, 5950) | Novel Protein sim. GBank gi 2392772 gb AAB70035_1 AAB7003 - (AC002534) putative chloroplast prephenate dehydratase [Arabidopsis thaliana] | | UNCLASSIFIED | 1053 |
| 7678 | 17672889 (22749, 22750) | Novel Protein sim. GBank gi 2408015 emb CAB16213_1 - (Z99162) hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1017 |
| 7679 | 11103035 (11249, 11250) | Novel Protein sim. GBank gi 2408224 (U93843) - HsdM [Klebsiella pneumoniae] | | UNCLASSIFIED | 1006, 1012 |
| 7680 | 20457009 (21863, 21864) | Novel Protein sim. GBank gi 2415399 (AF015775) - YodM [Bacillus subtilis] | | UNCLASSIFIED | 1010 |
| 7681 | 80076469 (1561, 1562) | Novel Protein sim. GBank gi 2429362 (AF020261) - proline rich protein [Santalum album] | | UNCLASSIFIED | 1034 |
| 7682 | 71047061 (22341, 22342) | Novel Protein sim. GBank gi 2429509 (AF025467) - contains similarity to drosophila DNA-binding protein K10 (NID:g6148) [Caenorhabditis elegans] | | UNCLASSIFIED | 1024 |
| 7683 | 36738341 (4193, 4194) | Novel Protein sim. GBank gi 2440104 emb CAB16677 - (Z99494) hypothetical protein MLCB57_37c [Mycobacterium leprae] | | UNCLASSIFIED | 1034 |
| 7684 | 65670184 (6729, 6730) | Novel Protein sim. GBank gi 2440127 emb CA09984 - (Z97182), lpqO [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1016 |
| 7685 | 87120503 (7739, 7740) | Novel Protein sim. GBank gi 2444165 (U91789) - Orf1 [Salmonella enteritidis] | | UNCLASSIFIED | 1025 |
| 7686 | 80079340 (5211, 5212) | Novel Protein sim. GBank gi 2467226 emb CAA63515 - (X92946) transposase [Lactococcus lactis] | | UNCLASSIFIED | 1034 |

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| 7687 | 80216283 (19879, 19880) | Novel Protein sim. G-Bank gi 2492823 sp Q12284 ERV2_YEAST - ERV2 PROTEIN PRECURSOR | | UNCLASSIFIED | 1003, 1004, 1006, 1008, 1010, 1022, 1024, 1026, 1031, 1034, 1039, 1044 |
| 7688 | 80027053 (13555, 13556) | Novel Protein sim. G-Bank gi 2492825 sp Q53389 AMB2_BACST - N- CARBAMYL-L-AMINO ACID AMIDOHYDROLASE | | UNCLASSIFIED | 1006, 1016 |
| 7689 | 79867740 (12095, 12096) | Novel Protein sim. G-Bank gi 2492900 sp Q04749 YMV8_YEAST - HYPOTHETICAL 47.1 KD PROTEIN IN NCA1- HMS1 INTERGENIC REGION | | UNCLASSIFIED | 1017 |
| 7690 | 32164246 (1585, 1586) | Novel Protein sim. G-Bank gi 2492932 sp Q46805 YGEY_ECOLI - HYPOTHETICAL 44.8 KD PROTEIN IN KDU1- LYSS INTERGENIC REGION | | UNCLASSIFIED | 1023 |
| 7691 | 21426257 (16551, 16552) | Novel Protein sim. G-Bank gi 2492945 sp Q58201 ARLY_METJA - ARGININOSUCCINATE LYASE (ARGININOSUCCINASE) (ASAL) | | UNCLASSIFIED | 1022 |
| 7692 | 9126181 (4203, 4204) | Novel Protein sim. G-Bank gi 2493550 sp Q02516 HAP5_YEAST - HAP5 TRANSCRIPTIONAL ACTIVATOR | | UNCLASSIFIED | 1006 |
| 7693 | 9383422 (5553, 5554) | Novel Protein sim. G-Bank gi 2494679 sp Q08193 YODO_YEAST - HYPOTHETICAL 51.9 KD PROTEIN IN MSE1- LAG2 INTERGENIC REGION PRECURSOR | | UNCLASSIFIED | 1017 |
| 7694 | 54994560 (11063, 11064) | Novel Protein sim. G-Bank gi 2494700 sp P76535 YFEU_ECOLI - HYPOTHETICAL 31.2 KD PROTEIN IN CYSP- AMIA INTERGENIC REGION | | UNCLASSIFIED | 1029 |
| 7695 | 70948830 (4571, 4572) | Novel Protein sim. G-Bank gi 2494701 sp Q45582 YBBI_BACSU - HYPOTHETICAL 33.0 KD PROTEIN YBBI | | UNCLASSIFIED | 1029 |

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| 7696 | 79859768 (19987, 19988) | Novel Protein sim. GBank gi 2495497 sp P77489 YAGR_ECOLI - HYPOTHETICAL 78.1 KD PROTEIN IN INTF-EAEH INTERGENIC REGION | UNCLASSIFIED | 1017 |
| 7697 | 29236487 (7323, 7324) | Novel Protein sim. GBank gi 2495569 sp Q57184 YDAO_HAEIN - HYPOTHETICAL PROTEIN H1371.1 | UNCLASSIFIED | 1026 |
| 7698 | 78980868 (7593, 7594) | Novel Protein sim. GBank gi 24955673 sp Q57534 Y321_HAEIN - HYPOTHETICAL PROTEIN H10321 | UNCLASSIFIED | 1016 |
| 7699 | 8900966 (14737, 14738) | Novel Protein sim. GBank gi 2496353 sp P75419 Y259_MYCPN - HYPOTHETICAL PROTEIN MG259 HOMOLOG | UNCLASSIFIED | 1004 |
| 7700 | 82454917 (12501, 12502) | Novel Protein sim. GBank gi 2496481 sp Q50724 Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78_27C | UNCLASSIFIED | 1001, 1012, 1022, 1023, 1027, 1031, 1039 |
| 7701 | 55281908 (17907, 17908) | Novel Protein sim. GBank gi 2496568 sp Q50603 Y0DD_MYCTU - HYPOTHETICAL 24.0 KD PROTEIN CY1A11.13C | UNCLASSIFIED | 1029, 1053 |
| 7702 | 30370138 (8293, 8294) | Novel Protein sim. GBank gi 2496730 sp P56606 Y4OU_RHISN - HYPOTHETICAL PROTEIN Y4OU PRECURSOR | UNCLASSIFIED | 1054 |
| 7703 | 10328691 (21887, 21888) | Novel Protein sim. GBank gi 2496818 sp Q10940 YW54_CAEEL - HYPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X | UNCLASSIFIED | 1025 |
| 7704 | 80020140 (4469, 4470) | Novel Protein sim. GBank gi 2497069 sp Q03760 YMK7_YEAST - URA5 INTERGENIC REGION | UNCLASSIFIED | 1008, 1009, 1017, 1022 |
| 7705 | 79855876 (8573, 8574) | Novel Protein sim. GBank gi 2497075 sp Q04511 YMI8_YEAST - HYPOTHETICAL 45.2 KD PROTEIN IN ZDS2-TUB1 INTERGENIC REGION | UNCLASSIFIED | 1017, 1022, 1044 |

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| 7706 | 214336666 (337, 338) | Novel Protein sim. GBank 9 2497110 sp Q04257 YMA3_YEAST - HYPOTHETICAL 34.0 KD PROTEIN IN GLO1-YPT7 INTERGENIC REGION | UNCLASSIFIED | 1022 |
| 7707 | 17295003 (15097, 15098) | Novel Protein sim. GBank 9 2497117 sp Q03690 IF31_YEAST - EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA) (EIF3 P135) (TRANSLATION INITIATION FACTOR EIF3, P135 SUBUNIT) | UNCLASSIFIED | 1039 |
| 7708 | 80219823 (13803, 13804) | Novel Protein sim. GBank 9 2497118 sp Q04347 YMP4_YEAST - HYPOTHETICAL 60.1 KD PROTEIN IN SEC59-ERG5 INTERGENIC REGION | UNCLASSIFIED | 1003, 1006, 1022, 1034, 1044 |
| 7709 | 30623969 (14909, 14910) | Novel Protein sim. GBank 9 2497121 sp Q04371 YMR7_YEAST - HYPOTHETICAL 54.1 KD PROTEIN IN PEX12-TAP42 INTERGENIC REGION | UNCLASSIFIED | 1022, 1026 |
| 7710 | 80500344 (489, 490) | Novel Protein sim. GBank 9 2497131 sp Q04659 YMT8_YEAST - HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION | UNCLASSIFIED | 1006, 1010, 1012, 1034 |
| 7711 | 82460247 (15431, 15432) | Novel Protein sim. GBank 9 2497136 sp Q04751 YMV9_YEAST - HYPOTHETICAL 32.3 KD PROTEIN IN NCA1-HMS1 INTERGENIC REGION | UNCLASSIFIED | 1001, 1022, 1025 |
| 7712 | 80219097 (2931, 2932) | Novel Protein sim. GBank 9 2497174 sp Q03218 YM43_YEAST - HYPOTHETICAL 56.2 KD PROTEIN IN SIP18-SPT21 INTERGENIC REGION | UNCLASSIFIED | 1001, 1022, 1025, 1034 |
| 7713 | 78799006 (4363, 4364) | Novel Protein sim. GBank 9 2497176 sp Q03220 YM45_YEAST - HYPOTHETICAL 37.0 KD PROTEIN IN SPT21-RGM1 INTERGENIC REGION | UNCLASSIFIED | 1022 |

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| 7714 | 39568538 (17349, 17350) | Novel Protein sim. GBank g 2497179 sp Q12751 YM48_YEAST - HYPOTHETICAL 113.2 KD PROTEIN IN SSO2-HSC82 INTERGENIC REGION | UNCLASSIFIED | 1006 |
| 7715 | 27955964 (18265, 18266) | Novel Protein sim. GBank g 2497179 sp Q12751 YM48_YEAST - HYPOTHETICAL 113.2 KD PROTEIN IN SSO2-HSC82 INTERGENIC REGION | UNCLASSIFIED | 1004, 1006, 1024, 1026 |
| 7716 | 27988945 (22367, 22368) | Novel Protein sim. GBank g 2497206 sp Q04806 YM85_YEAST - HYPOTHETICAL 42.4 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION | UNCLASSIFIED | 1016 |
| 7717 | 29024399 (16313, 16314) | Novel Protein sim. GBank g 2497213 sp Q03508 YM8F_YEAST - HYPOTHETICAL 54.1 KD PROTEIN IN TPS3-IPP2 INTERGENIC REGION | UNCLASSIFIED | 1017 |
| 7718 | 80507435 (9381, 9382) | Novel Protein sim. GBank g 2497226 sp Q04869 YM94_YEAST - HYPOTHETICAL 38.2 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION | UNCLASSIFIED | 1012, 1025, 1039 |
| 7719 | 79115547 (6747, 6748) | Novel Protein sim. GBank g 2497617 sp Q633313 LBP_RAT - LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) | UNCLASSIFIED | 1003 |
| 7720 | 17927241 (7501, 7502) | Novel Protein sim. GBank g 2497947 sp P74840 PRPD_SALTY - PRPD PROTEIN | UNCLASSIFIED | 1038 |
| 7721 | 8490635 (3491, 3492) | Novel Protein sim. GBank g 2497997 sp Q12175 MSH5_MUTS - PROTEIN HOMOLOG 5 | UNCLASSIFIED | 1024 |
| 7722 | 82125189 (20655, 20656) | Novel Protein sim. GBank g 2498064 sp Q12746 YMM5_YEAST - HYPOTHETICAL 35.3 KD PROTEIN IN HMGS-TUB3 INTERGENIC REGION | UNCLASSIFIED | 1006, 1008, 1016, 1022, 1023, 1024, 1034 |
| 7723 | 19738760 (1233, 1234) | Novel Protein sim. GBank g 2498298 sp Q12387 DEC1_YEAST - DEC1 PROTEIN (MDM20 PROTEIN) | UNCLASSIFIED | 1001 |

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| 7724 9126) | 25541197 (9125, Novel Protein sim. GBank gii2498410 spl Q12315 GLE1_YEAST - RNA EXPORT FACTOR GLE1 | | UNCLASSIFIED | 1009 |
| 7725 66694411 (4349, 4350) | Novel Protein sim. GBank gii2498414 spl Q484811 GLF8_KLEPN - PROBABLE UDP-GALACTOPYRANOSE MUTASE | | UNCLASSIFIED | 1009 |
| 7726 27837972 (4471, 4472) | Novel Protein sim. GBank gii2498438 spl Q12060 HFI1_YEAST - TRANSCRIPTIONAL COACTIVATOR HFI1/ADA1 | | UNCLASSIFIED | 1006 |
| 7727 57299540 (7835, 7836) | Novel Protein sim. GBank gii2498477 spl Q06706 IK13_YEAST - IK13 PROTEIN | | UNCLASSIFIED | 1012, 1017, 1022, 1024, 1026, 1034 |
| 7728 86692192 (10737, 10738) | Novel Protein sim. GBank gii2498477 spl Q06706 IK13_YEAST - IK13 PROTEIN | | UNCLASSIFIED | 1018 |
| 7729 79176918 (12859, 12860) | Novel Protein sim. GBank gii2498788 spl Q0615861PLSB_MOUSE - GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) (P90) | | UNCLASSIFIED | 1024 |
| 7730 11759311 (11471, 11472) | Novel Protein sim. GBank gii2498993 spl Q08314 TGT_HELPY - QUEUINE TRNA-RIBOSYLYL TRANSFERASE (TRNA - GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) | | UNCLASSIFIED | 1024 |
| 7731 78898837 (16583, 16584) | Novel Protein sim. GBank gii2499125 spl Q07878 VP13_YEAST - VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13 | | UNCLASSIFIED | 1017 |
| 7732 79862148 (21471, 21472) | Novel Protein sim. GBank gii2499125 spl Q07878 VP13_YEAST - VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13 | | UNCLASSIFIED | 1008, 1009, 1022, 1023, 1025, 1034, 1038, 1039 |

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| 7733 | 78753190 (9101, 9102) | Novel Protein sim. GBank gi 2499126 sp Q12194 YP66_YEAST - HYPOTHETICAL 54.9 KD PROTEIN IN VPS28-BTS1 INTERGENIC REGION | | UNCLASSIFIED | 1008, 1044 |
| 7734 | 17292485 (11409, 11410) | Novel Protein sim. GBank gi 2499481 sp Q49092 YBL3_MORCA-HYPOTHETICAL 46.4 KD PROTEIN IN BL0R-1 3'REGION (ORF3) | | UNCLASSIFIED | 1039 |
| 7735 | 8490481 (3581, 3582) | Novel Protein sim. GBank gi 2499966 sp Q4128 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A) | | UNCLASSIFIED | 1034 |
| 7736 | 80071069 (10247, 10248) | Novel Protein sim. GBank gi 2501040 sp Q05814 SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS) | | UNCLASSIFIED | 1010, 1031 |
| 7737 | 79116389 (21605, 21606) | Novel Protein sim. GBank gi 2501167 sp P7133 YHGF_HAEIN - HYPOTHETICAL PROTEIN H10568 | | UNCLASSIFIED | 1013 |
| 7738 | 79569002 (17669, 17670) | Novel Protein sim. GBank gi 2501514 sp Q64324 STX2_MOUSE - SYNTAXIN BINDING PROTEIN 2 (UNC-18 HOMOLOG 2) (UNC-18B) (MUSEC1) | | UNCLASSIFIED | 1004 |
| 7739 | 27974545 (5775, 5776) | Novel Protein sim. GBank gi 2501571 sp Q02891 YP95_YEAST - HYPOTHETICAL 51.7 KD PROTEIN IN SEC62-MSY1 INTERGENIC REGION | | UNCLASSIFIED | 1004 |
| 7740 | 66727316 (20067, 20068) | Novel Protein sim. GBank gi 2501583 sp Q55156 Y064_SYNY3 - HYPOTHETICAL 43.0 KD PROTEIN SLR0064 | | UNCLASSIFIED | 1049 |
| 7741 | 19515814 (17869, 17870) | Novel Protein sim. GBank gi 2501593 sp Q57981 Y531_METJA - HYPOTHETICAL PROTEIN MJ0531 | | UNCLASSIFIED | 1024 |

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| 7742 | 39434881 (6483, 6484) | Novel Protein sim. GBank gi 2501738 sp Q06639 YD03_YEAST - PUTATIVE 101.7 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN PRO1-CPR5 INTERGENIC REGION | UNCLASSIFIED | 1010, 1024 |
| 7743 | 66397374 (6619, 6620) | Novel Protein sim. GBank gi 2506132 sp P36683 ACO2_ECOLI - ACCONITATE HYDRATASE 2 (CITRATE HYDROLASE 2) (ACCONITASE 2) | UNCLASSIFIED | 1008 |
| 7744 | 91235299 (18345, 18346) | Novel Protein sim. GBank gi 2506139 sp P249661 COPD_ORYSA - COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) | UNCLASSIFIED | 1003 |
| 7745 | 80021107 (1979, 1980) | Novel Protein sim. GBank gi 2506393 sp P31576 FIXX_ECOLI - FERREDOXIN LIKE PROTEIN | UNCLASSIFIED | 1024 |
| 7746 | 117939502 (15333, 15334) | Novel Protein sim. GBank gi 2506465 sp P39811 GLR2_ECOLI - GLUTAREDOXIN 2 (GRX2) | UNCLASSIFIED | 1039 |
| 7747 | 79640300 (2399, 2400) | Novel Protein sim. GBank gi 2506493 sp P38036 YGCGB_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH1 INTERGENIC REGION | UNCLASSIFIED | 1039 |
| 7748 | 80054815 (13895, 13896) | Novel Protein sim. GBank gi 2506625 sp P52697 YBHE_ECOLI - HYPOTHETICAL 36.3 KD PROTEIN IN MODCB10A INTERGENIC REGION | UNCLASSIFIED | 1022 |
| 7749 | 25315630 (63, 64) | Novel Protein sim. GBank gi 2506765 sp P47029 YJ14_YEAST - HYPOTHETICAL 117.2 KD PROTEIN IN EXO70-ARP4 INTERGENIC REGION | UNCLASSIFIED | 1009 |
| 7750 | 88064332 (10935, 10936) | Novel Protein sim. GBank gi 2506915 sp P21769 ODFP_RAT - OUTER DENSE FIBER PROTEIN (RT7 PROTEIN) (RT5/1) | UNCLASSIFIED | 1008, 1017 |

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| 7751 | 79612632 (139, 140) | Novel Protein sim. GBank gil2506975 spl P15272 AMN_ECOLI - AMP NUCLEOSIDASE | | UNCLASSIFIED | 1022 |
| 7752 | 46899493 (22217, 22218) | Novel Protein sim. GBank gil2506985 spl P50851 CC4H_HUMAN - CDC4-LIKE PROTEIN | | UNCLASSIFIED | 1040 |
| 7753 | 79429507 (9707, 9708) | Novel Protein sim. GBank gil2507147 spl P22257 TIG_ECOLI - TRIGGER FACTOR (TF) | | UNCLASSIFIED | 1017 |
| 7754 | 20727950 (13309, 13310) | Novel Protein sim. GBank gil2507295 spl P39199 YFCB_ECOLI - HYPOTHETICAL ADENINE-SPECIFIC METHYLASE IN AROCF-FADL INTERGENIC REGION | | UNCLASSIFIED | 1006 |
| 7755 | 79452313 (17921, 17922) | Novel Protein sim. GBank gil2507347 spl P04050 RPB1_YEAST - DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (B220) | | UNCLASSIFIED | 1010, 1024 |
| 7756 | 80500925 (20841, 20842) | Novel Protein sim. GBank gil2507511 spl P37340 YDHE_ECOLI - HYPOTHETICAL 19.4 KD PROTEIN IN RIBC-PYKF INTERGENIC REGION | | UNCLASSIFIED | 1012 |
| 7757 | 80223858 (1479, 1480) | Novel Protein sim. GBank gil253435 bb bs 110869 - (S42186) Vps35p [Saccharomyces cerevisiae=yeast, Peptide, 937 aa] [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1003, 1004, 1006, 1009, 1022, 1024 |
| 7758 | 8486607 (14063, 14064) | Novel Protein sim. GBank gil2559004 (AF026269) - prominin [Mus musculus] | | UNCLASSIFIED | 1022 |
| 7759 | 66370567 (19587, 19588) | Novel Protein sim. GBank gil2578444 emb CAA47812 - (X67427) pba [Pisum sativum] | | UNCLASSIFIED | 1054 |
| 7760 | 79963875 (17209, 17210) | Novel Protein sim. GBank gil2580435 db IBAA23140 - (D76414) N-acetylglucosaminidase [Staphylococcus aureus] | | UNCLASSIFIED | 1022 |

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| 7761 | 11131459 (5193, 5194) | Novel Protein sim. GBank gi 2612821 emb CAA04438 - (AJ000978) cis/trans isomerase [Pseudomonas putida] | UNCLASSIFIED | 1024 |
| 7762 | 24137026 (22867, 22868) | Novel Protein sim. GBank gi 2612821 emb CAA04438 - (AJ000978) cis/trans isomerase [Pseudomonas putida] | UNCLASSIFIED | 1003 |
| 7763 | 78184018 (8411, 8412) | Novel Protein sim. GBank gi 2619000 (AF027868) - YoaT [Bacillus subtilis] | UNCLASSIFIED | 1053 |
| 7764 | 16280147 (11715, 11716) | Novel Protein sim. GBank gi 2621084 (AE000797) - conserved protein [Methanobacterium thermoautotrophicum] | UNCLASSIFIED | 1054 |
| 7765 | 80071744 (19397, 19398) | Novel Protein sim. GBank gi 2622039 (AE000868) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum] | UNCLASSIFIED | 1022, 1026 |
| 7766 | 57306083 (1373, 1374) | Novel Protein sim. GBank gi 2622565 (AE000906) - unknown [Methanobacterium thermoautotrophicum] | UNCLASSIFIED | 1006, 1029 |
| 7767 | 46741764 (7493, 7494) | Novel Protein sim. GBank gi 2632005 emb CAA05565 - (AJ002571) YkaA [Bacillus subtilis] | UNCLASSIFIED | 1054 |
| 7768 | 79628516 (3083, 3084) | Novel Protein sim. GBank gi 2632009 emb CAA05568 - (AJ002571) Y'kCB [Bacillus subtilis] | UNCLASSIFIED | 1039 |
| 7769 | 78677252 (13097, 13098) | Novel Protein sim. GBank gi 2632162 emb CAA04544 - (AJ001118) monoglyceride lipase [Mus musculus] | UNCLASSIFIED | 1022 |
| 7770 | 85818137 (1141, 1142) | Novel Protein sim. GBank gi 2632362 emb CAB11871 - (Z99104) similar to hypothetical proteins [Bacillus subtilis] | UNCLASSIFIED | 1019 |
| 7771 | 46660015 (5991, 5992) | Novel Protein sim. GBank gi 2633555 emb CAB13058 - (Z99110) similar to fructose phosphotransferase system enzyme II [Bacillus subtilis] | UNCLASSIFIED | 1029 |

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| 7772 | 30194801 (19993, 19994) | Novel Protein sim. GBank gil2633555 emb CAB13058 - (Z99110) similar to fructose phosphotransferase system enzyme II [Bacillus subtilis] | UNCLASSIFIED | 1026 |
| 7773 | 20458631 (16819, 16820) | Novel Protein sim. GBank gil2633811 emb CAB13333 - (Z99111) phosphotransferase system (PTS) fructose-specific enzyme IIBC component [Bacillus subtilis] | UNCLASSIFIED | 1010 |
| 7774 | 78478222 (3845, 3846) | Novel Protein sim. GBank gil2634069 emb CAB13570 - (Z99112) similar to hypothetical proteins [Bacillus subtilis] | UNCLASSIFIED | 1038 |
| 7775 | 23331942 (10069, 10070) | Novel Protein sim. GBank gil2642157 (AC003000) - ankyrin-like protein [Arabidopsis thaliana] | UNCLASSIFIED | 1029 |
| 7776 | 65503327 (11607, 11608) | Novel Protein sim. GBank gil2645205 (J63648) - p160 myb-binding protein [Mus musculus] | UNCLASSIFIED | 1022, 1023 |
| 7777 | 28592723 (20547, 20548) | Novel Protein sim. GBank gil2649977 (AE001060) - conserved hypothetical protein [Archaeoglobus fulgidus] | UNCLASSIFIED | 1044 |
| 7778 | 78617042 (15245, 15246) | Novel Protein sim. GBank gil2650410 (AE001090) - glutamine ABC transporter, periplasmic glutamine-binding protein (GlnH) [Archaeoglobus fulgidus] | UNCLASSIFIED | 1039 |
| 7779 | 80250210 (18941, 18942) | Novel Protein sim. GBank gil2650749 (AE001114) - A. fulgidus predicted coding region AF2347 [Archaeoglobus fulgidus] | UNCLASSIFIED | 1006 |
| 7780 | 86674147 (12387, 12388) | Novel Protein sim. GBank gil2661856 emb CAB06301 - (Z83933) protoporphyrin IX Mg chelatase encoding subunit of 144 kDa [Chlorobium vibrioforme] | UNCLASSIFIED | 1026, 1029 |
| 7781 | 65586309 (6079, 6080) | Novel Protein sim. GBank gil2662165 dbj BAA23714 - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens] | UNCLASSIFIED | 1024, 1031 |

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| 7782 | 66644385 (6219, 6220) | Novel Protein sim. GBank gj 26662165 dbj [BAA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens] | | UNCLASSIFIED | |
| 7783 | 66002941 (13563, 13564) | Novel Protein sim. GBank gj 266346 sp Q01292 ILV5_SPO1 - KETOL-ACID REDUCTOISOMERASE PRECURSOR (ACETOHYDROXY-ACID REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE) | | UNCLASSIFIED | 1003 |
| 7784 | 78895542 (15773, 15774) | Novel Protein sim. GBank gj 266859 sp Q01329 PTA1_YEAST - PTA1 PROTEIN | | UNCLASSIFIED | 1039 |
| 7785 | 65451776 (19467, 19468) | Novel Protein sim. GBank gj 266859 sp Q01329 PTA1_YEAST - PTA1 PROTEIN | | UNCLASSIFIED | 1016 |
| 7786 | 78736132 (18201, 18202) | Novel Protein sim. GBank gj 2673972 AC002561 - unknown protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1003, 1017 |
| 7787 | 10067356 (949, 950) | Novel Protein sim. GBank gj 267439 sp P11288 YAAA_ECOLI - HYPOTHETICAL 29.6 KD PROTEIN IN THRC-TALB INTERGENIC REGION | | UNCLASSIFIED | 1044 |
| 7788 | 28780390 (20403, 20404) | Novel Protein sim. GBank gj 267497 sp P30267 YKAA_BACFI - HYPOTHETICAL 50.9 KD PROTEIN IN KATA 3'REGION (ORF A) | | UNCLASSIFIED | 1022 |
| 7789 | 80047436 (1239, 1240) | Novel Protein sim. GBank gj 26888556 (AE001164) - vacuolar X-prolyl dipeptidyl aminopeptidase I (pepX) [Borrelia burgdorferi] | | UNCLASSIFIED | 1004, 1034 |
| 7790 | 20369375 (7893, 7894) | Novel Protein sim. GBank gj 269582 emb CA-A15890 - (AL021006) hypothetical protein Rv1234 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1004 |

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| 7791 | 30407879 (15065, 15066) | Novel Protein sim. GBank gil 26959541 emb [CAA15847] - (AL010186) hypothetical protein Rv1170 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1026 |
| 7792 | 11094040 (18347, 18348) | Novel Protein sim. GBank gil 2708667 (AF037441) - putative 19.5 kDa protein [Edwardsiella ictaluri] | UNCLASSIFIED | 1022 |
| 7793 | 20428302 (21037, 21038) | Novel Protein sim. GBank gil 2738164 (U91842) - hypothetical protein [Bacillus firmus] | UNCLASSIFIED | 1010 |
| 7794 | 20456914 (15561, 15562) | Novel Protein sim. GBank gil 2760909 (AF036925) - Family 10 xylanase [Candidatusisruptor sp. Rf69B.1] | UNCLASSIFIED | 1010 |
| 7795 | 11695905 (12909, 12910) | Novel Protein sim. GBank gil 2764825 emb [CAA66092] - (X97452) paaC [Escherichia coli] | UNCLASSIFIED | 1034 |
| 7796 | 20751341 (585, 586) | Novel Protein sim. GBank gil 2765047 emb [CAA71110] - (Y09990) putative RNaseE homologue [Salmonella typhi] | UNCLASSIFIED | 1053 |
| 7797 | 11684107 (10331, 10332) | Novel Protein sim. GBank gil 2766551 (AF040104) - polyosecharide export protein [Rhizobium leguminosarum bv. trifoli] | UNCLASSIFIED | 1016 |
| 7798 | 8910955 (11753, 11754) | Novel Protein sim. GBank gil 2772619 (U93355) - hypothetical 32.1 kDa protein [Erwinia herbicola] | UNCLASSIFIED | 1017 |
| 7799 | 78460104 (13233, 13234) | Novel Protein sim. GBank gil 2791420 emb [CAA16014.1] - (AL021185) ppsS [Mycobacterium tuberculosis] | UNCLASSIFIED | 1026 |
| 7800 | 54817140 (5215, 5216) | Novel Protein sim. GBank gil 2791495 emb [CAA16032] - (AL021246) hypothetical protein Rv2455c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1029 |
| 7801 | 11695477 (13129, 13130) | Novel Protein sim. GBank gil 2791510 emb [CAA16047] - (AL021246) gibO [Mycobacterium tuberculosis] | UNCLASSIFIED | 1034 |

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| 7802 | 51628181 (16371, 16372), Novel Protein sim. GBank gil2791635 emb CAA16122..11 - (AL021287) hypothetical protein Rv3037c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1040 |
| 7803 | 65460236 (239, 240), Novel Protein sim. GBank gil27917 emb CAA73543 - (Y13095) ORF142 [Staphylococcus sciuri] | | UNCLASSIFIED | 1016 |
| 7804 | 80079357 (7451, 7452), Novel Protein sim. GBank gil2804624 (U89347) - malonate decarboxylase gamma subunit [Acinetobacter calcoaceticus] | | UNCLASSIFIED | 1034 |
| 7805 | 20729449 (19857, 19858), Novel Protein sim. GBank gil2811044 sp O06250 Y115..MYCTU - HYPOTHETICAL 46.9 KD PROTEIN CY77.05C | | UNCLASSIFIED | 1006 |
| 7806 | 78466439 (2219, 2220), Novel Protein sim. GBank gil2815604 (AF025438) - Opa-interacting protein OIP2 [Homo sapiens] | | UNCLASSIFIED | 1026 |
| 7807 | 80021193 (14507, 14908), Novel Protein sim. GBank gil2826874 emb CAA76168 - (Y16311) SpoQJ-like protein [Streptomyces coelicolor] | | UNCLASSIFIED | 1006, 1022, 1024, 1039 |
| 7808 | 78460855 (15407, 15408), Novel Protein sim. GBank gil2828292 emb CAA16706..11 - (AL021687) neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1044 |
| 7809 | 65472844 (11551, 11552), Novel Protein sim. GBank gil282950 sp P71550 YT14..MYCTU - HYPOTHETICAL 13.9 KD PROTEIN CY10D7..14C | | UNCLASSIFIED | 1023 |
| 7810 | 82060865 (4467, 4468), Novel Protein sim. GBank gil2829815 sp P95095 CSTA..MYCTU - CARBON STARVATION PROTEIN A HOMOLOG | | UNCLASSIFIED | 1004, 1006, 1010, 1012, 1016, 1024 |
| 7811 | 33764003 (19789, 19790), Novel Protein sim. GBank gil2829890 (AC002396) - Hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1026 |

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| 7812 | 29444855 (11263, 11264) | Novel Protein sim. GBank gi 2829910 (AC002291) - Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana] | UNCLASSIFIED | 1026 |
| 7813 | 87892765 (15689, 15690) | Novel Protein sim. GBank gi 282994 pir S27762 - Sip1 protein - barley | UNCLASSIFIED | 1025 |
| 7814 | 65855363 (3851, 3852) | Novel Protein sim. GBank gi 2833221 spi Q12214 HOS1_YEAST - HOS1 PROTEIN | UNCLASSIFIED | 1003, 1006, 1022, 1024 |
| 7815 | 78455768 (12259, 12260) | Novel Protein sim. GBank gi 2833225 spi Q12299 NOP5_YEAST - NUCLEOLAR PROTEIN NOP5 | UNCLASSIFIED | 1026 |
| 7816 | 80381812 (18483, 18484) | Novel Protein sim. GBank gi 2833311 spi Q2-828 YNFD_CAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5_13 IN CHROMOSOME II | UNCLASSIFIED | 1029 |
| 7817 | 79776510 (5085, 5086) | Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken | UNCLASSIFIED | 1008, 1025, 1030, 1050 |
| 7818 | 11077819 (5599, 55600) | Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken | UNCLASSIFIED | 1024 |
| 7819 | 80243856 (9737, 9738) | Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken | UNCLASSIFIED | 1001, 1004, 1022, 1024 |
| 7820 | 20447603 (4607, 4608) | Novel Protein sim. GBank gi 2842445 emb CAA11813 - (AJ224072) histone 1 [Mytilus edulis] | UNCLASSIFIED | 1024 |
| 7821 | 10219102 (11817, 11818) | Novel Protein sim. GBank gi 284775 pir S27870 - house-keeping protein - mouse | UNCLASSIFIED | 1004 |
| 7822 | 32303167 (1089, 1090) | Novel Protein sim. GBank gi 2852636 (AF007155) - unknown [Homo sapiens] | UNCLASSIFIED | 1029 |
| 7823 | 8490182 (10035, 10036) | Novel Protein sim. GBank gi 285303 pir A42261 - heparan sulfate proteoglycan - rat | UNCLASSIFIED | 1024 |
| 7824 | 66002613 (2887, 2898) | Novel Protein sim. GBank gi 2853599 (AF031898) - CheZ [Pseudomonas putida] | UNCLASSIFIED | 1003, 1010 |

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| 7825 | 80222147 (4409, 4410) | Novel Protein sim. GBank gil2854158[gb]AAC02577.1 - (AF045641) No definition line found [Caenorhabditis elegans] | UNCLASSIFIED | 1006, 1009, 1022 |
| 7826 | 28389737 (15949, 15950) | Novel Protein sim. GBank gil285953[dbj]BAA03498 - (D14664) KIAA0022 [Homo sapiens] | UNCLASSIFIED | 1003, 1044 |
| 7827 | 32723325 (14957, 14968) | Novel Protein sim. GBank gil288590[emb]CAA48159.1 - (X68020) ARP [Saccharomyces cerevisiae] | UNCLASSIFIED | 1001 |
| 7828 | 21661213 (14079, 14080) | Novel Protein sim. GBank gil2894206[emb]CAA17072 - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1024 |
| 7829 | 91226994 (4187, 4188) | Novel Protein sim. GBank gil2894612[emb]CAA17146 - (AL021889) putative protein [Arabidopsis thaliana] | UNCLASSIFIED | 1010 |
| 7830 | 9945895 (7063, 7064) | Novel Protein sim. GBank gil2894795 (U76907) - 17 kDa common-antigen [Rickettsia sp.] | UNCLASSIFIED | 1044 |
| 7831 | 20286920 (12301, 12302) | Novel Protein sim. GBank gil2896719[emb]CAA17198.1 - (AL021897) hypothetical protein Rv1082 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1034 |
| 7832 | 79430083 (5869, 5870) | Novel Protein sim. GBank gil2900497 (L10328) - f562 [Escherichia coli] | UNCLASSIFIED | 1017 |
| 7833 | 77523099 (22081, 22082) | Novel Protein sim. GBank gil2909643[emb]CAA17455 - (AL021942) hypothetical protein Rv0584 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1023 |
| 7834 | 86473942 (14193, 14194) | Novel Protein sim. GBank gil2911072[emb]CAA17534.1 - (AL021960) putative protein [Arabidopsis thaliana] | UNCLASSIFIED | 1054 |
| 7835 | 65704798 (6615, 6616) | Novel Protein sim. GBank gil291688[emb]CAA17629.1 - (AL022004) hypothetical protein Rv0823c [Mycobacterium tuberculosis] | UNCLASSIFIED | 1023 |
| 7836 | 47656865 (2111, 2112) | Novel Protein sim. GBank gil2920641 (AF044503) - hcp [Escherichia coli] | UNCLASSIFIED | 1029 |

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| 7837 | 25266008 (17317) 17318) | Novel Protein sim. GBank gi 2921422 (AF036677) - unknown [Salmonella typhimurium] | | UNCLASSIFIED | 1054 |
| 7838 | 8911583 (5195, 5196) | Novel Protein sim. GBank gi 292463 emb CAA17703 - (AL022021) hypothetical protein Rv7781c [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1003 |
| 7839 | 24138405 (10129, 10130) | Novel Protein sim. GBank gi 2947228 (AF031886) - erythrocyte binding protein [Plasmodium yoelii yoelli] | | UNCLASSIFIED | 1003 |
| 7840 | 30003965 (19331, 19332) | Novel Protein sim. GBank gi 2952522 (AF051357) - golgin-245 [Mus musculus] | | UNCLASSIFIED | 1016, 1022 |
| 7841 | 79627701 (12111, 12112) | Novel Protein sim. GBank gi 29525271 gb AAC05772.1 - (AF051356) putative hemolysin [Streptococcus mutans] | | UNCLASSIFIED | 1001 |
| 7842 | 29691795 (19947, 19948) | Novel Protein sim. GBank gi 29525281 gb AAC05773.1 - (AF051356) pyruvate-formate lyase activating enzyme [Streptococcus mutans] | | UNCLASSIFIED | 1024 |
| 7843 | 78798387 (3031, 3032) | Novel Protein sim. GBank gi 295616 (M24378) - IRAI [Saccharomyces cerevisiae] | | UNCLASSIFIED | 1022 |
| 7844 | 70451483 (13197, 13198) | Novel Protein sim. GBank gi 2956769 emb CAA17882.1 - (AL022103) phosphatidylinositol phosphate phosphatase; synaptosomal-like [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1049 |
| 7845 | 94939107 (2045, 2046) | Novel Protein sim. GBank gi 2960107 emb CAA18005.1 - (AL022121) hypothetical protein Rv3683 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1012 |
| 7846 | 80183435 (12791, 12792) | Novel Protein sim. GBank gi 2970646 (AF051945) - Xin [Mus musculus] | | UNCLASSIFIED | 1001, 1022 |
| 7847 | 80084754 (13053, 13054) | Novel Protein sim. GBank gi 2970646 (AF051945) - Xin [Mus musculus] | | UNCLASSIFIED | 1001 |
| 7848 | 10159775 (16073, 16074) | Novel Protein sim. GBank gi 2970646 (AF051945) - Xin [Mus musculus] | | UNCLASSIFIED | 1001 |

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| 7849 | 29346130 (9281, 9282) | Novel Protein sim. GBank gi 2980781 emb CAA18208.1 - (AL02219B) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1022 |
| 7850 | 79820669 (5125, 5126) | Novel Protein sim. GBank gi 2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | | UNCLASSIFIED | 1039 |
| 7851 | 24135395 (6119, 6120) | Novel Protein sim. GBank gi 2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | | UNCLASSIFIED | 1003 |
| 7852 | 29265223 (6879, 6880) | Novel Protein sim. GBank gi 2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | | UNCLASSIFIED | 1022 |
| 7853 | 866673455 (9117, 9118) | Novel Protein sim. GBank gi 2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | | UNCLASSIFIED | 1007 |
| 7854 | 6626611 (21651, 21652) | Novel Protein sim. GBank gi 2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | | UNCLASSIFIED | 1022 |
| 7855 | 66489048 (22713, 22714) | Novel Protein sim. GBank gi 2981631 dbj BAA25253.1 - (AB012223) ORF2 [Canis familiaris] | | UNCLASSIFIED | 1029 |
| 7856 | 86694604 (525, 526) | Novel Protein sim. GBank gi 2983010 (AE000684) - glutamate racemase [Aquifex aeolicus] | | UNCLASSIFIED | 1018 |
| 7857 | 80502803 (8839, 8840) | Novel Protein sim. GBank gi 2983039 (AE000686) - proline-tRNA synthetase [Aquifex aeolicus] | | UNCLASSIFIED | 1012 |
| 7858 | 78472450 (19865, 19866) | Novel Protein sim. GBank gi 2983116 (AE000690) - hypothetical protein [Aquifex aeolicus] | | UNCLASSIFIED | 1044 |
| 7859 | 78784143 (843, 844) | Novel Protein sim. GBank gi 2983213 (AE000697) - mannose-6-phosphate isomerase/mannose-1- phosphate guanyl transferase [Aquifex aeolicus] | | UNCLASSIFIED | 1006, 1022, 1031 |
| 7860 | 85523012 (16153, 16154) | Novel Protein sim. GBank gi 2983357 (AE000708) - pantothenate metabolism flavoprotein [Aquifex aeolicus] | | UNCLASSIFIED | 1049 |

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| 7861 | 65707960 (8035, 8036) | Novel Protein sim. GBank gil29842222 (AE000766) - fuculose-1-phosphate aldolase [Aquilifex aeolicus] | | UNCLASSIFIED | 1023 |
| 7862 | 80249025 (8811, 8812) | Novel Protein sim. GBank gil2995312 emb CAA18340 - (AL022268) hypothetical protein SC4H2.25 [Streptomyces coelicolor] | | UNCLASSIFIED | 1003, 1004, 1006, 1010 |
| 7863 | 20458553 (17827, 17828) | Novel Protein sim. GBank gil299532 emb CAA04606.1 - (AJ001206) pep1 [Streptomyces coelicolor] | | UNCLASSIFIED | 1010 |
| 7864 | 20474031 (137, 138) | Novel Protein sim. GBank gil299650 (AC004493) - KIAA0324 [Homo sapiens] | | UNCLASSIFIED | 1004, 1010 |
| 7865 | 25328221 (22311, 22312) | Novel Protein sim. GBank gil2997593 (AF020816) - glucose-6-phosphate/phosphate-translocator precursor [Solanum tuberosum] | | UNCLASSIFIED | 1008 |
| 7866 | 87466974 (9189, 9190) | Novel Protein sim. GBank gil3023275 spi Q43763 AGLU_HORVU - ALPHA- GLUCOSIDASE PRECURSOR (MALTASE) | | UNCLASSIFIED | 1025 |
| 7867 | 39384799 (11597, 11598) | Novel Protein sim. GBank gil3023717 spi Q08649 ESA1_YEAST - ESA1 PROTEIN | | UNCLASSIFIED | 1034 |
| 7868 | 20288062 (18607, 18608) | Novel Protein sim. GBank gil30248372 spi Q55790 Y074_SYNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074 | | UNCLASSIFIED | 1034 |
| 7869 | 19746688 (9269, 9270) | Novel Protein sim. GBank gil3025061 spi P75949 YCFO_ECOLI - HYPOTHETICAL 37.6 KD PROTEIN IN FHUE- NDH INTERGENIC REGION | | UNCLASSIFIED | 1039 |
| 7870 | 79842574 (10157, 10158) | Novel Protein sim. GBank gil3025094 spi Q03835 YD98_YEAST - BMH2 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1008, 1017, 1039 |
| 7871 | 79833832 (21747, 21748) | Novel Protein sim. GBank gil3025094 spi Q03835 YD98_YEAST - HYPOTHETICAL 32.5 KD PROTEIN IN MSH6- BMH2 INTERGENIC REGION | | UNCLASSIFIED | 1003, 1008, 1017 |

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| 7872 | 8491792 (22965, 22966) | Novel Protein sim. GBank gi 3025215 sp Q18486 YLC4_CAEEL - HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III | | UNCLASSIFIED | 1022 |
| 7873 | 25328743 (21973, 21974) | Novel Protein sim. GBank gi 3025282 sp P7691 YR40_MYCTU - HYPOTHETICAL 35.8 KD PROTEIN CY21B4.40 | | UNCLASSIFIED | 1008 |
| 7874 | 34080752 (2149, 2150) | Novel Protein sim. GBank gi 3043548 dbj BA25438 - (AB011084) KIAA0512 protein [Homo sapiens] - No definition line found [Arabidopsis thaliana] | | UNCLASSIFIED | 1000 |
| 7875 | 86473919 (9041, 9042) | Novel Protein sim. GBank gi 3047114 (AF058919) putative [Escherichia coli] | | UNCLASSIFIED | 1054 |
| 7876 | 86678808 (22677, 22678) | Novel Protein sim. GBank gi 304931 (L17086) - putative [Escherichia coli] | | UNCLASSIFIED | 1007 |
| 7877 | 37034876 (9545, 9546) | Novel Protein sim. GBank gi 3063877 emb CAA18562 - (AL022486) putative integral membrane protein [Mycobacterium leprae] | | UNCLASSIFIED | 1012 |
| 7878 | 10054330 (20143, 20144) | Novel Protein sim. GBank gi 3080473 emb CAA18668 - (AL022602) udp-n- acetylglucosamine->n-acetylglucosaminyl - (pentapeptide) pyrophosphoryl-undecaprenol n- acetylglucosamine transferase [Mycobacterium leprae] | | UNCLASSIFIED | 1012 |
| 7879 | 77967677 (20237, 20238) | Novel Protein sim. GBank gi 3080500 emb CAA18697 - (AL022602) hypothetical protein MLCB268_31c [Mycobacterium leprae] | | UNCLASSIFIED | 1036 |
| 7880 | 66043054 (5827, 5828) | Novel Protein sim. GBank gi 3080530 emb CAA18658 - (AL022600) hypothetical protein [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1016 |
| 7881 | 17898362 (13573, 13574) | Novel Protein sim. GBank gi 3080767 (AF041381) - putative transcriptional repressor E2F-6 [Homo sapiens] | | UNCLASSIFIED | 1044 |

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| 7882 | 17884279 (15611, 15612) | Novel Protein sim. GBank gil3114661 (AF061267) - putative alpha-ketoglutarate-dependent hydrophosphite dioxygenase [Pseudomonas stutzeri] | UNCLASSIFIED | 1039 |
| 7883 | 78406525 (4977, 4978) | Novel Protein sim. GBank gil31223141isp1Q34971 KDPD_RATRA - SENSOR PROTEIN KDPD | UNCLASSIFIED | 1016 |
| 7884 | 79864487 (18177, 18178) | Novel Protein sim. GBank gil31224041isp1Q06225 MURC_MYCTU - UDP-N-ACETYL MURAMATE--ALANINE LIGASE (UDP-N-ACETYL MURANOYL-L-ALANINE SYNTHETASE) | UNCLASSIFIED | 1012 |
| 7885 | 78380245 (9285, 9286) | Novel Protein sim. GBank gil31229051isp1Q26687 SYM_METTH-METHIONYL-TRNA SYNTHETASE (METHIONINE-TRNA LIGASE) (METRS) | UNCLASSIFIED | 1000, 1008, 1026, 1029 |
| 7886 | 11291349 (16705, 16706) | Novel Protein sim. GBank gil31229821isp1Q12093 TRMU_YEAST - PROBABLE TRNA (5'-METHYLAMINOMETHYL-2'-THIOURIDYLATE)-METHYLTRANSFERASE | UNCLASSIFIED | 1022 |
| 7887 | 27984611 (13209, 13210) | Novel Protein sim. GBank gil31229821isp1Q12093 TRMU_YEAST - PROBABLE TRNA (5'-METHYLAMINOMETHYL-2'-THIOURIDYLATE)-METHYLTRANSFERASE | UNCLASSIFIED | 1008, 1034 |
| 7888 | 20436829 (14787, 14788) | Novel Protein sim. GBank gil31230141isp1P87498 VIT1_CHICK - VITELLOGENIN I PRECURSOR (MINOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LV1); PHOSVTIN (PV); LIPOVITELLIN II (LVII); YGP42] | UNCLASSIFIED | 1010 |
| 7889 | 80061727 (6313, 6314) | Novel Protein sim. GBank gil3123021isp1Q80508 VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VITG_I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVTIN (PV); LIPOVITELLIN 2 (LV2)) | UNCLASSIFIED | 1024 |

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| 7890 9996) | 80243196 (9995, 9996) | Novel Protein sim. GBank g 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025 | | UNCLASSIFIED | 1001, 1004, 1009, 1022, 1024, 1044 |
| 7891 15042) | 78768175 (15041, 15042) | Novel Protein sim. GBank g j3123209 sp P23039 EFG1_YEAST - ELONGATION FACTOR G, MITOCHONDRIAL 1 PRECURSOR (MEF-G-1) | | UNCLASSIFIED | 1017, 1022 |
| 7892 22126) | 32302888 (22125, 22126) | Novel Protein sim. GBank g 3128208_AC004077 - hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1029 |
| 7893 15196) | 78920553 (15195, 15196) | Novel Protein sim. GBank g 3128218_AC004077 - putative end13 protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1039 |
| 7894 4474) | 97981207 (4473, 4474) | Novel Protein sim. GBank g 3128374_AF010496 - hypothetical protein [Rhodobacter capsulatus] | | UNCLASSIFIED | 1031 |
| 7895 13352) | 37805818 (13351, 13352) | Novel Protein sim. GBank g 3128382_AF013282 - MmTbx14 [Mus musculus] | | UNCLASSIFIED | 1058 |
| 7896 18164) | 57280237 (18163, 18164) | Novel Protein sim. GBank g 3135267_AC003058 - hypothetical protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1034 |
| 7897 17916) | 20708130 (17915, 17916) | Novel Protein sim. GBank g j3142214 dbj BAA28327 _ (AB010150) mannosyltransferase [Escherichia coli] | | UNCLASSIFIED | 1053 |
| 7898 3526) | 27996632 (3525, 3526) | Novel Protein sim. GBank g 3142291_AC002411 - Contains similarity to adenylylate cyclase gb AF012921 from Magnaporthe griseae. EST gb Z224512 comes from this gene. [Arabidopsis thaliana] | | UNCLASSIFIED | 1030 |
| 7899 1046) | 19881159 (1045, 1046) | Novel Protein sim. GBank g 3153821_AF062655 - plenty-of-prolines-101; POP10; SH3-philo- protein [Mus musculus] | | UNCLASSIFIED | 1034 |
| 7900 15340) | 86477499 (15339, 15340) | Novel Protein sim. GBank g 3153821_AF062655 - plenty-of-prolines-101; POP10; SH3-philo- protein [Mus musculus] | | UNCLASSIFIED | 1029 |

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| 7901 | 82401801 (3917, 3918) | Novel Protein sim. GBank gi 3169721 gb AAC17939.1 - (AF007569) GsrR [Bradyrhizobium leponicum] | | UNCLASSIFIED | 1001, 1038 |
| 7902 | 78073994 (16735, 16736) | Novel Protein sim. GBank gi 3170887 (AF061555) - ubiquitin-protein ligase E3-alpha [Mus musculus] | | UNCLASSIFIED | 1024 |
| 7903 | 78675661 (9921, 9922) | Novel Protein sim. GBank gi 3183285 sp P77649 YD1U_ECOLI - HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION | | UNCLASSIFIED | 1022 |
| 7904 | 27973628 (19483, 19484) | Novel Protein sim. GBank gi 3183285 sp P77649 YD1U_ECOLI - HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION | | UNCLASSIFIED | 1053 |
| 7905 | 80023962 (561, 562) | Novel Protein sim. GBank gi 3182438 sp P77774 YFGL_ECOLI - HYPOTHETICAL 41.9 KD PROTEIN IN XSEA-HISS INTERGENIC REGION | | UNCLASSIFIED | 1053 |
| 7906 | 20467859 (9553, 9554) | Novel Protein sim. GBank gi 3183489 sp Q06489 YP18_YEAST - HYPOTHETICAL 45.0 KD PROTEIN IN PIS1-CLB2 INTERGENIC REGION | | UNCLASSIFIED | 1010 |
| 7907 | 17868673 (3007, 3008) | Novel Protein sim. GBank gi 3184082 emb CAA19338 - (AL02378) - N-terminal acetyltransferase 1 [Schizosaccharomyces pombe] | | UNCLASSIFIED | 1024 |
| 7908 | 27986043 (5589, 5590) | Novel Protein sim. GBank gi 3191996 emb CAA19395 - (AL02379) hypothetical protein SC2E1.20 [Streptomyces coelicolor] | | UNCLASSIFIED | 1006 |
| 7909 | 56149085 (9999, 10000) | Novel Protein sim. GBank gi 3193284 (AF069298) - No definition line found [Arabidopsis thaliana] | | UNCLASSIFIED | 1003 |
| 7910 | 11399346 (21849, 21850) | Novel Protein sim. GBank gi 3193327 (AF069299) - No definition line found [Arabidopsis thaliana] | | UNCLASSIFIED | 1006 |

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| 7911 | 11769816 (19519, 19520) | Novel Protein sim. GBank gi 3212996 gb AAC23433.1 - (AC004997) match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), T59198 (NID:g661035), and AA027979 (NID:g1494038) [Homo sapiens] | UNCLASSIFIED | 1016 |
| 7912 | 388861267 (15877, 15878) | Novel Protein sim. GBank gi 322752 pir A44226 - auxin-independent growth promoter - Nicotiana tabacum | UNCLASSIFIED | 1026 |
| 7913 | 80019495 (421, 422) | Novel Protein sim. GBank gi 3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana] | UNCLASSIFIED | 1006, 1023, 1024, 1034 |
| 7914 | 14994658 (3651, 3652) | Novel Protein sim. GBank gi 3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana] | UNCLASSIFIED | 1027 |
| 7915 | 57514736 (11335, 11336) | Novel Protein sim. GBank gi 3242705 (AC003040) - putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana] | UNCLASSIFIED | 1001, 1006, 1009, 1024, 1026 |
| 7916 | 39559043 (15043, 15044) | Novel Protein sim. GBank gi 3256023 emb CAA17228.1 - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis] | UNCLASSIFIED | 1008 |
| 7917 | 87466650 (17647, 17648) | Novel Protein sim. GBank gi 325605 dbj BAA29288.1 - (AP000001) 125aa long hypothetical protein [Pyrococcus horikoshii] | UNCLASSIFIED | 1015 |
| 7918 | 82375773 (14609, 14610) | Novel Protein sim. GBank gi 325605 dbj BAA29289.1 - (AP000001) 171aa long hypothetical protein [Pyrococcus horikoshii] | UNCLASSIFIED | 1001, 1006 |
| 7919 | 19424875 (12551, 12552) | Novel Protein sim. GBank gi 325608 dbj BA429291.1 - (AP000001) 235aa long hypothetical protein [Pyrococcus horikoshii] | UNCLASSIFIED | 1054 |

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| 7920 | 78919297 (15079, 15080) | Novel Protein sim. GBank gi 3256779 dbj BA29462 - (AP000002) 422aa long hypothetical protein [Pyrococcus horikoshii] | | UNCLASSIFIED | 1008 |
| 7921 | 79554658 (18475, 18476) | Novel Protein sim. GBank gi 3257120 dbj BA29803 - (AP000003) 230aa long hypothetical protein [Pyrococcus horikoshii] | | UNCLASSIFIED | 1039 |
| 7922 | 79810415 (5301, 5302) | Novel Protein sim. GBank gi 3258173 dbj BA30856.1 - (AP000007) 306aa long hypothetical UDP-glucose 4-epimerase [Pyrococcus horikoshii] | | UNCLASSIFIED | 1008 |
| 7923 | 11809488 (10017, 10018) | Novel Protein sim. GBank gi 3261489 emb CAA15488 - (AL008687) speE [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1022 |
| 7924 | 87899077 (21423, 21424) | Novel Protein sim. GBank gi 3261523 emb CAA17328 - (AL021928) mmpL3 [Mycobacterium tuberculosis] | | UNCLASSIFIED | 1015 |
| 7925 | 38916141 (14009, 14010) | Novel Protein sim. GBank gi 3281846 emb CAA07004 - (AJ006404) late elongated hypocotyl [Arabidopsis thaliana] | | UNCLASSIFIED | 1026 |
| 7926 | 79815120 (6499, 6500) | Novel Protein sim. GBank gi 3282044 emb CAA74300 - (Y13967) alpha- amino adipate reductase large subunit [Penicillium chrysogenum] | | UNCLASSIFIED | 1044 |
| 7927 | 35933503 (15729, 15730) | Novel Protein sim. GBank gi 3282331 (AF072100) - GalR-Lac homolog, PxS [Pseudomonas aeruginosa] | | UNCLASSIFIED | 1053 |
| 7928 | 65660774 (18057, 18058) | Novel Protein sim. GBank gi 3287876 sp P72349 NDAD_ALCXX - D- AMINOACYLASE (N-ACYL-D-AMINO-ACID DEACYLASE) | | UNCLASSIFIED | 1041 |
| 7929 | 12902105 (16365, 16366) | Novel Protein sim. GBank gi 3292814 emb CAA19804.11 - (AL031018) putative protein [Arabidopsis thaliana] | | UNCLASSIFIED | 1031, 1050 |
| 7930 | 79844169 (18589, 18590) | Novel Protein sim. GBank gi 3294467 (U89341)- phosphoglucomutase 1 [Zea mays] | | UNCLASSIFIED | 1017, 1022, 1026, 1039 |